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TITLE: Y2H56 A strong IKK binding protein

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U.S. PATENT DOCUMENTS

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	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5776717	July 1998	Cao	435/15
☐	5804374	September 1998	Baltimore et al.	435/6

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ART-UNIT: 162

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ABSTRACT:

The present invention provides an isolated I.kappa.B kinase binding protein designated Y2H56 and functional equivalents therof. The amino acid sequence of Y2H56, the nucleotide sequence encoding Y2H56, and other related protein and nucleic acid molecules are also provided.

8 Claims, 0 Drawing figures
Exemplary Claim Number: 1

BRIEF SUMMARY:

1 BACKGROUND OF THE INVENTION

2 Extracellular stimuli associated with immune responses, inflammatory responses, and apoptosis activate kinases through receptor mediated processes. Ashkenazi and Dixit, Science 281, 1305-1308 (1998). For example,

inflammatory cytokines such as tumor necrosis factor .alpha. (TNF.alpha.) or interleukin-1 (IL-1), activate kinases which in turn activate NF-.kappa.B by phosphorylating inhibitory proteins known as I.kappa.Bs. Phosphorylation of I.kappa.Bs is a key regulatory step for NF-.kappa.B mediated processes. See, for example, Baeuerle and Henkel, Annu. Rev. Immunol. 12, 141-179 (1994); Baldwin, Annu. Rev. Immunol. 14, 649-683 (1996); Siebenlist et al., Annu. Rev. Cell Biol. 12, 405-455 (1994); and Verma et al, Genes Dev. 9, 2723-2735 (1995). The kinases that phosphorylate I.kappa.Bs are called I.kappa.B kinases (IKKs).

3 The determination and characterization of kinases involved in signaling pathways leading to, for example, immune, inflammatory, and apoptotic responses is important for understanding and controlling these processes. Recently, an I.kappa.B kinase, designated IKK.alpha. but also referred to as CHUK (conserved helix-loop-helix ubiquitous kinase), was identified in a yeast-two-hybrid screen with NIK as bait. Regnier et al., Cell 90, 373-383 (1997). IKK.alpha. was determined to be responsible for the major I.kappa.B kinase activity induced by TNF stimulation of HeLa cells. DiDonato et al., Nature 388, 548-554 (1997). The identification of IKK.alpha. as a cytoplasmic kinase which phosphorylates I.kappa.B family members at their physiologically relevant sites and targets them for proteosome-mediated degradation was a major breakthrough.

4 The IKK.alpha. gene encodes a 745 amino-acid polypeptide (having a molecular mass of approximately 85 kDa). Murine and human IKK.alpha. cDNA clones were found to be almost identical. Connelly and Marcu, Cellular and Molecular Biology Research 41, 537-549 (1995).

5 Another kinase, termed IKK.beta., homologous to IKK.alpha., has also been reported. Stancovski and Baltimore, Cell 91, 299-302 (1997); Woronicz et al., Science 278, 866-869 (1997); and Zandi et al., Cell 91, 243-252 (1997). IKK.alpha. and IKK.beta. have 52% overall similarity to each other and 65% identity in the kinase domain. Zandi et al., Cell 91, 243-252 (1997). An I.kappa.B kinase termed T2K has also been described in U.S. Pat. No. 5,776,717 to Cao.

6 The known I.kappa.B protein kinases generally phosphorylate I.kappa.Bs at specific serine residues. For example, they specifically phosphorylate serines 32 and 36 of I.kappa.B.alpha.. Phosphorylation of both sites is required to efficiently target I.kappa.B.alpha. for destruction in vivo. Moreover, activation of IKK.alpha. and IKK.beta. occurs in response to NF-.kappa.B activating agents and mutant IKK.alpha. and IKK.beta. that are catalytically inactive block NF-.kappa.B stimulation by cytokines. These results highlight the important role played by I.kappa.B protein kinases in NF-.kappa.B activation processes. See Stancovski and Baltimore, Cell 91, 299-302 (1997) for a recent discussion of I.kappa.B kinases.

7 IKK.alpha. and IKK.beta., have structural motifs characteristic of the IKK kinases. This includes an amino terminal serine-threonine kinase domain separated from a carboxyl proximal helix-loop-helix (H-L-H) domain by a leucine zipper domain. These structural characteristics are unlike other kinases, and the domains are thought to be involved in protein-protein interactions.

8 Numerous proteins are involved in the signaling pathways that lead to immune, inflammatory, and apoptotic responses. A complete elucidation of these processes requires the identification of additional proteins that are involved and a determination of the protein interactions.

9 The discovery of additional proteins involved in these processes is important for controlling immune, apoptotic, and inflammatory processes. Thus, there is a great need for the identification and characterizion of additional proteins involved in IKK mediated cellular processes.

10 SUMMARY OF THE INVENTION

11 The present invention provides an isolated IKK binding protein comprising the amino acid sequence set forth in SEQ ID NO:1 and functional equivalents thereof Also included are isolated nucleic acid molecules that encode the IKK binding protein comprising the amino acid sequence set forth in SEQ ID NO:1 and its functional equivalents, methods of making the IKK binding proteins comprising expressing nucleic acid molecules encoding the proteins, and antibodies directed to the IKK binding proteins.

12 DETAILED DESCRIPTION OF THE INVENTION

13 The invention is directed to an IKK binding protein, designated Y2H56, and its functional equivalents. Y2H56 will hereinafter refer to the protein defined by SEQ ID NO:1, which is found in humans.

14 In this specification, functional equivalents are proteins or fragments that are substantially homologous to SEQ ID NO:1 and that specifically bind to an IKK protein, such as IKK.alpha. or IKK.beta.. The term IKK is used herein to refer to all kinases that phosphorylate any I.kappa.B and that have helix-loop-helix and leucine zipper domains. Y2H56 and its functional equivalents bind to the region of the IKK proteins made up of the contiguous helix-loop-helix and leucine zipper domains.

15 In order to determine whether the sequence of a first protein, or fragment thereof, is substantially homologous to the sequence of a second protein, such as Y2H56, or fragment thereof, the sequences are first aligned so as to optimize the percent of amino acid residues that are identical, or that are identical or equivalent, at corresponding positions. Gaps may be introduced in the sequences, if necessary, to achieve optimization.

16 Amino acids generally considered to be equivalent are indicated below in separate rows (a) through (e):

17 (a) Ala (A), Ser (S), Thr (T), Pro (P), Gly (G)

18 (b) Asn (N), Asp (D), Glu (E), Gln (Q)

19 (c) His (H), Arg (R), Lys (K)

20 (d) Met (M), Leu (L), Ile (I), Val (V)

21 (e) Phe (F), Tyr (Y), Trp (W)

22 The amino acid sequences of highly homologous proteins can usually be aligned by visual inspection. If visual inspection is insufficient, the proteins are aligned in accordance with any of the methods described by George, D. G. et al, in Macromolecular Sequencing and Synthesis, Selected Methods and Applications, pages 127-149, Alan R. Liss, Inc. (1988), such as the formula described at page 137 using a match score of 1, a mismatch score of 0, and a gap penalty of -1.

23 In a first embodiment, the sequence of a protein or fragment thereof is considered substantially homologous to the sequence of Y2H56 or a fragment thereof if the amino acid sequences, after alignment, are at least about 25% identical, preferably at least about 35% identical, more preferably at least about 50% identical, even more preferably at least about 65% identical, still more preferably at least about 75% identical, most preferably at least about 85% identical, and, ideally at least about 95% identical.

24 In a second embodiment, the sequence of a protein or fragment thereof is considered substantially homologous to the sequence of Y2H56 or a fragment thereof if the amino acid sequences, after alignment, are at least about 50%

identical or equivalent, preferably at least about 65% identical or equivalent, most preferably at least about 85% identical or equiavalent, and ideally at least about 95% identical or equivalent.

25 Functional equivalents include all modifications of the polypeptide set forth in SEQ ID NO:1. These modifications may be introduced deliberately, as by site-directed mutagenesis, or may be natural variations and mutations. Such modifications include substitutions, additions, and/or deletions in the protein sequences as long as substantial homology and specific binding to IKK proteins are maintained.

26 For example, functional equivalents include variant Y2H56 proteins that are expressed by naturally occurring alleles. Alleles are alternative forms of a gene that occupy a given locus of a chromosome within a species.

27 Functional equivalents of Y2H56 also include proteins from non-human mammalian species (species orthologs) as well as proteins expressed by alleles of such species orthologs. Non-human mammals include, for example, primates, pet animals such as dogs and cats, laboratory animals such as rats and mice, and farm animals such as horses, sheep, and cows.

28 The proteins of the invention that do not occur in nature are isolated. The term "isolated" as used herein, in the context of proteins, refers to a polypeptide which is unaccompanied by at least some of the material with which it is associated in its natural state. The isolated protein constitutes at least 0.5%, preferably at least 5%, more preferably at least 25% and still more preferably at least 50% by weight of the total protein in a given sample.

29 Most preferably the "isolated" protein is substantially free of other

30 proteins, lipids, carbohydrates or other materials with which it is naturally associated, and yields a single major band on a non-reducing polyacrylamide gel. Substantially free means that the protein is at least 75%, preferably at least 85%, more preferably at least 95% and most preferably at least 99% free of other proteins, lipids, carbohydrates or other materials with which it is naturally associated.

31 The invention also provides novel and/or isolated nucleic acid molecules ~~that~~ encode SEQ ID NO:1 and the functional equivalents thereof. Nucleic acid molecules (nucleic acids) of the invention include deoxyribonucleic acid (DNA), complementary DNA (cDNA), and ribonucleic acid (RNA) sequences.

32 For example, the invention includes an isolated nucleic acid molecule as set forth in ~~either SEQ ID NO:2 or SEQ ID NO:3, isolated nucleic acid molecules that are substantially homologous with~~ SEQ ID NO:2 or SEQ ID NO:3, isolated nucleic acid molecules that hybridize with SEQ ID NO:2 or SEQ ID NO:3 under stringent conditions, nucleic acid sequences that are degenerate as a result of the genetic code, and the complements and fragments thereof.

33 In order to determine whether the sequence of a first nucleic acid molecule, or fragment thereof, is substantially homologous to the sequence of a second nucleic acid molecule, such as SEQ ID NO:2, or fragment thereof, the sequences are first aligned so as to optimize the percent of nucleotides that are identical at corresponding positions. Gaps may be introduced in the sequences if necessary to achieve optimization.

34 The nucleic acid sequences of highly homologous nucleic acid molecules can usually be aligned by visual inspection. If visual inspection is insufficient, the nucleic acid molecules are aligned in accordance with any of the methods described by George, D. G. et al, in Macromolecular Sequencing and Synthesis, Selected Methods and Applications, pages 127-149, Alan R. Liss, Inc. (1988), such as the formula described at page 137 using a

match score of 1, a mismatch score of 0, and a gap penalty of -1.

35 In the present specification, the sequence of a nucleic acid molecule or fragment thereof is considered substantially homologous to SEQ ID NO:2, or a fragment thereof, if the nucleic acid sequences, after alignment, are at least about 40% identical, preferably at least about 50% identical, more preferably at least about 60% identical, even more preferably at least about 70% identical, still more preferably at least about 80% identical, most preferably at least about 90% identical, and, ideally at least about 95% identical.

36 The invention also includes nucleic acid molecules that hybridize to SEQ ID NO:2 or SEQ ID NO:3, a fragment of SEQ ID NO:2, a complement of SEQ ID NO:2, or a complement of a fragment of SEQ ID NO:2 under stringent conditions. Also included in the invention are a preferred group of protein functional equivalents of SEQ ID NO:1 encoded by nucleic acid molecules that hybridize under stringent conditions to a sequence complementary to SEQ ID NO:2 or a fragment of SEQ ID NO:2.

37 The term "stringent conditions," as used herein, is equivalent to "high stringent conditions" and "high stringency." These terms are used interchangeably in the art.

38 Stringent conditions are defined in a number of ways. In one definition, stringent conditions are selected to be about 50.degree. C. lower than the thermal melting point (T.sub.m) for a specific sequence at a defined ionic strength and pH. The T.sub.m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched sequence. Typical stringent conditions are those in which the salt concentration is about 0.02 M at pH 7 and the temperature is at least about 60.degree. C. Further examples of stringent conditions can be found in U.S. Pat. No. 5,789,550 to Goeddel et al. (1998). The description of stringent conditions in U.S. Pat. No. 5,789,550 is herein incorporated by reference.

39 Stringent conditions, in the nucleic acid hybridization context, include a combination of conditions, such as the nature and concentration of salts and organic solvents, temperature, and other parameters that are typically known to control hybridization reactions. The combination of parameters is more important than the measure of any single parameter. See U.S. Pat. No. 5,786,210; Wetmur and Davidson, J. Mol. Biol. 31, 349-370 (1968). Generally, stringent conditions are obtained at higher temperatures and lower ionic strength. Control of hybridization conditions, and the relationships between hybridization conditions and degree of homology are understood by those skilled in the art. See, for example, Bej, A. K., Nucleic Acid Hybridizations: Principles and Strategies, in Dangler, C. A. ed, Nucleic Acid Analysis:

40 Principles and Bioapplications, Wiley-Liss, Inc., pp. 1-29 (1996); Adams et al., The Biochemistry of the Nucleic Acids, pp. 605-606, Chapman & Hall (1992); Sambrook J, Fritsch EF, and Maniatis T, Molecular Cloning. A Laboratory Manual, 2d ed., Cold Spring Harbor Laboratory, Cold Spring Harbor (1989).

41 Fragments of nucleic acid molecules of the invention include primers and probes which are useful as tools in molecular biology and biotechnology. The fragment may or may not encode a polypeptide that binds to IKK.alpha. or IKK.beta.. Even if the encoded polypeptide does not bind, the fragment can be used, for example, as a primer ("amplimer") to selectively amplify nucleic acid, such as genomic DNA or total RNA. Primers can also be used in nucleic acid amplification procedures such as the polymerase chain reaction (PCR), ligase chain reaction (LCR), repair chain reaction (RCR), PCR oligonucleotide ligation assay (PCR-OLA), and the like.

42 Fragments of the nucleic acid molecules of the invention can also be oligonucleotides complementary to a target nucleic acid molecule, i.e., the fragment can be a probe. Such oligonucleotides can be DNA or RNA. Oligonucleotides useful as probes in hybridization studies, such as in situ hybridization, can also be constructed.

43 The length of the oligonucleotide probe is not critical, as long as it is capable of hybridizing to the target molecule. The oligonucleotide should contain at least 6 nucleotides, preferably at least 10 nucleotides, and more preferably, at least 15 nucleotides. There is no upper limit to the length of the oligonucleotide probes. Longer probes are more difficult to prepare and require longer hybridization times. Therefore, the probe should not be longer than necessary. Normally, the oligonucleotide probe will not contain more than 50 nucleotides, preferably not more than 40 nucleotides, and, more preferably, not more than 30 nucleotides.

44 Numerous methods for detectably labeling such probes with radioisotopes, fluorescent tags, enzymes, binding moieties (e.g., biotin), and the like are known, so that the probes of the invention can be adapted for easy detectability. Methods for making and using nucleic acid probes are understood by those skilled in the art. See, for example, Keller G H and Manak M M, DNA Probes, 2d ed., Macmillan Publishers Ltd., England (1991) and Hames B D and Higgins S J, eds., Gene Probes I and Gene Probes II, IRL Press, Oxford (1995).

45 The nucleic acid molecules may contain synthetic sequences that do not occur in nature and/or they are isolated. The term "isolated," as used herein, in the context of nucleic acids, includes nucleic acid molecules unaccompanied by at least some of the material with which they are associated in their natural state. The isolated nucleic acid may constitute at least 0.5%, preferably at least 5%, more preferably at least 25% and still more preferably at least 50% by weight of the total nucleic acid in a given sample.

46 Most preferably the "isolated" nucleic acid is substantially free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which it is naturally associated. Substantially free means that the nucleic acid is at least 75%, preferably at least 85%, more preferably at least 95% and most preferably at least 99% free of other nucleic acids, proteins, lipids, carbohydrates or other materials with which it is naturally associated. The nucleic acid molecules of the invention can also be recombinant, meaning that they comprise a non-natural sequence or a natural sequence joined to nucleotide(s) other than than those in which they are joined on the natural chromosome.

47 Y2H56 was shown, using yeast two-hybrid screens, to bind to the carboxyl terminal domain regions of IKK.alpha. and IKK.beta.. See example 1. Y2H56 specifically binds with the region of the IKK proteins made up of the contiguous helix-loop-helix and leucine zipper domains. The binding of the Y2H56 protein to the IKKs is stronger than the binding of IKK.alpha. to a natural substrate of IKK.alpha., viz. I.kappa.BP.beta.2.

48 The Y2H56 protein and the other IKK.alpha. binding proteins described in example 1 are useful for elucidating and controlling pathways leading to inflammation and apoptosis. These processes are mediated by receptors such as tumor necrosis factor (TNF) receptors. The IKK binding proteins can also be used to detect IKK complexes and modulate IKK activity in cells undergoing signalling by inflammatory mediators such as TNF.alpha. and Il-1.

49 The Y2H56 protein and its functional equivalents are also useful for identifying therapeutically active agents that modulate the binding or interaction of Y2H56 and either IKK.alpha. or IKK.beta.. Such agents can either prevent the formation of Y2H56/IKK complexes or prevent or inhibit the dissociation of Y2H56/IKK complexes. Molecules that prevent the

formation of Y2H56/IKK complexes or inhibit the dissociation of these complexes are useful for boosting the immune system, or as immunosuppresants, or as antiinflammatory agents.

50 Complex formation or dissociation can be determined by methods well known in the art. Such methods include, for example, gel filtration, sucrose density gradient centrifugation, crosslinking, and immunoprecipitation.

51 The proteins and variants of the proteins can be prepared by methods known in the art. Such methods include isolating the protein directly from cells, and synthesizing the protein chemically from individual amino acids. Preferably, the proteins of the invention can be prepared by providing DNA that encodes the protein, amplifying or cloning the DNA, expressing the DNA in a suitable host, and harvesting the protein.

52 DNA encoding the proteins of the invention can be synthesized or isolated. The DNA of the invention can be synthesized chemically from the four nucleotides in whole or in part by methods known in the art. Such methods include those described by Caruthers, Science 230, 281-285 (1985). DNA can also be synthesized by preparing overlapping double-stranded oligonucleotides, filling in the gaps, and ligating the ends together. See, generally, Sambrook et al. (1989) and Glover D M and Hames B D, eds., DNA Cloning, 2d ed., Vols. 1-4, IRL Press, Oxford (1995).

53 DNA expressing functional homologs of the protein can be prepared from wild-type DNA by site-directed mutagenesis. See, for example, Zoller and Smith, Nucleic Acids Res 10, 6487-6500 (1982); Zoller, Methods Enzymol 100, 468-500 (1983); Zoller, DNA 3(6), 479-488 (1984); and McPherson, ed., Directed Mutagenesis: A Practical Approach, IRL Press, Oxford (1991).

54 DNA encoding the protein of the invention can be isolated from different species by using the human sequence, SEQ ID NO:2, to prepare one or more oligonucleotide probes. The probe is labeled and used to screen a genornic or cDNA library in a suitable vector, such as phage lambda. The homology between the DNA of the Y2H56 of the species being screened and that of the human DNA is taken into account in determining the conditions of hybridization. The cDNA library may be prepared from MnRNA by known methods, such as those described in Gubler and Hoffman, Gene 25, 263-270 (1983). Oligonucleotide probes can be used to screen cDNA libraries from different species and tissues. The oligonucleotide probe should be labeled so that it can be detected upon hybridization to DNA in the library being screened. These methods are well known in the art.

55 The DNA isolated is sequenced, and the sequence used to prepare additional oligonucleotide probes. This procedure may be repeated to obtain overlapping fragments until a complete open reading frame is produced.

56 The nucleic acids of the invention may be amplified by methods known in the art. One suitable method is the polymerase chain reaction (PCR) method described by Saiki et al., Science 239, 487 (1988), Mullis et al in U.S. Pat. No. 4,683,195 and by Sambrook et al. (1989). It is convenient to amplify the clones in the lambda-gt10 or lambda-gt11 vectors using lambda-gt10 or lambda-gt11-specific oligomers as the amplimers (available from Clontech, Palo Alto, Calif.). Other amplification procedures that are well known in the art such as ligase chain reaction (LCR), repair chain reaction (RCR), and PCR oligonucleotide ligation assay (PCR-OLA) can also be used to amplify the nucleic acids of the invention.

57 DNA encoding the proteins of the invention, or unique fragments thereof, may also be cloned in a suitable host cell and expressed by methods well known in the art. The DNA and protein may be recovered from the host cell. See, generally, Sambrook et al. (1989), for methods relating to the manufacture and manipulation of nucleic acids. The entire gene or additional fragments of the gene can be isolated by using the known DNA sequence or a fragment

thereof as a probe. To do so, restriction fragments from a genomic or cDNA library may be identified by Southern hybridization using labeled oligonucleotide probes derived from SEQ ID NO:2.

58 The amplified or cloned DNA can be expressed in a suitable expression vector by methods known in the art. See, generally, Sambrook et al. (1989).

59 A variety of expression vectors and host cell systems can be used. These include, for example, microorganisms such as bacteria transformed with recombinant bacteriophage DNA, plasmid DNA, or cosmid DNA containing the Y2H56 coding region. Other expression vectors and host cell systems that can be used include yeast transformed with recombinant yeast expression vectors containing the Y2H56 coding sequence, insect cells infected with recombinant virus expression vectors containing the Y2H56 coding sequence, plant cells infected with recombinant virus expression vectors containing the Y2H56 coding sequence, or animal cells infected with recombinant virus expression vectors (e.g., retroviruses, adenovirus, vaccinia virus) containing the Y2H56 coding sequence.

60 The expression vectors useful in the present invention contain at least one expression control sequence that is operatively linked to the DNA sequence or fragment to be expressed. The control sequence is inserted in the vector in order to control and to regulate the expression of the cloned DNA sequence. Examples of useful expression control sequences are the lac system, the trp system, the tac system, the trc system, major operator and promoter regions of phage lambda, the control region of fd coat protein, the glycolytic promoters of yeast, e.g., the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, e.g., Pho5, the promoters of the yeast alpha-mating factors, and promoters derived from polyoma, adenovirus, retrovirus, and simian virus, e.g., the early and late promoters or SV40, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells and their viruses or combinations thereof.

61 Useful expression hosts include well-known prokaryotic and eukaryotic cells. Some suitable prokaryotic hosts include, for example, E. coli, such as E. coli SG-936, E. coli HB 101, E. coli W3110, E. coli X1776, E. coli X2282, E. coli DHI, and E. coli MRC1, Pseudomonas sp., Bacillus sp., such as B. subtilis, and Streptomyces sp. Suitable eukaryotic cells include yeasts and other fungi, insect, animal cells, such as COS cells and CHO cells, human cells and plant cells in tissue culture.

62 Preferably, Y2H56 is expressed using baculoviral vectors in insect cell cultures. In general, the transformation of insect cells and production of foreign proteins therein is disclosed in Guarino et al., U.S. Pat. No. 5,162,222.

63 Proteins can be isolated from a solubilized fraction by standard methods. Some suitable methods include precipitation and liquid chromatographic protocols such as ion exchange, hydrophobic interaction, and gel filtration. See, for example, Methods Enzymol (Guide to Protein Chemistry, Deutscher, ed., Section VII) pp. 182:309 (1990) and Scopes, Protein Purification, Springer-Verlag, New York (1987), which are herein incorporated by reference.

64 Alternatively, purified material is obtained by separating the protein on

65 preparative SDS-PAGE gels, slicing out the band of interest and electroeluting the protein from the polyacrylamide matrix by methods known in the art. The detergent SDS is removed from the protein by known methods, such as by dialysis or the use of a suitable column, such as the Extracti-Gel column from Pierce. Mixtures of proteins can be separated by, for example, SDS-PAGE in accordance with the method of Laemmli, Nature 227, 680-685 (1970). Such methods are well known in the art.

66 The proteins of the invention can also be chemically synthesized by methods known in the art. Suitable methods for synthesizing proteins are described by Stuart and Young, Solid Phase Peptide Synthesis, 2d ed., Pierce Chemical Company (1984).

67 The invention also includes antibodies or antibody fragments that specifically bind to epitopes of the proteins of the invention defined by the amino acid sequence set forth in SEQ ID NO:1. An "antibody" in accordance with the present specification is defined broadly as a protein that binds specifically to an epitope. The antibodies of the invention can be monoclonal antibodies, polyclonal antibodies, chimerized antibodies, humanized antibodies, single chain antibodies, or a fragment thereof For use in in vivo applications with human subjects, the antibody is preferably chimerized or humanized, containing an antigen binding region from, e.g., a rodent, with the bulk of the antibody replaced with sequences derived from human immunoglobulin.

68 Antibodies further include recombinant polyclonal or monoclonal Fab fragments prepared in accordance with the method of Huse et al., Science 246, 1275-1281 (1989).

69 Polyclonal antibodies are isolated from mammals that have been inoculated with the protein or a functional analog in accordance with methods known in the art. Briefly, polyclonal antibodies may be produced by injecting a host mammal, such as a rabbit, mouse, rat, or goat, with the protein or a fragment thereof capable of producing antibodies that distinguish between mutant and wild-type protein. The peptide or peptide fragment injected may contain the wild-type sequence or the mutant sequence. Sera from the mammal are extracted and screened to obtain polyclonal antibodies that are specific to the peptide or peptide fragment.

70 The antibodies are preferably monoclonal. Monoclonal antibodies may be produced by methods known in the art. These methods include the immunological method described by Kohler and Milstein, Nature 256:495-497 (1975) and by Campbell, in Burdon et al., eds, Laboratory Techniques in Biochemistry and Molecular Biology, Vol. 13, Elsevier Science Publishers, Amsterdam (1985); as well as the recombinant DNA method described by Huse et al.(1989).

71 To produce monoclonal antibodies, a host mammal is inoculated with a peptide or peptide fragment as described above, and then boosted. Spleens are collected from inoculated mammals a few days after the final boost. Cell suspensions from the spleens are fused with a tumor cell in accordance with the general method described by Kohler and Milstein (1975). See also Campbell (1985). To be usefull, a peptide fragment must contain sufficient amino acid residues to define the epitope of the molecule being detected.

72 If the fragment is too short to be immunogenic, it may be conjugated to a carrier molecule. Some suitable carrier molecules include keyhole limpet hemocyanin and bovine serum albumin. Conjugation may be carried out by methods known in the art. One such method is to combine a cysteine residue of the fragment with a cysteine residue on the carrier molecule.

73 Methods for making chimeric and humanized antibodies are also known in the art. For example, antibodies can be engineered using genetic techniques to produce chimeric antibodies including protein components from two or more species.

74 For example, methods for making chimeric antibodies include those described in U.S. patents by Boss (Celltech) and by Cabilly (Genentech). See U.S. Pat. Nos. 4,816,397 and 4,816,567, respectively. Methods for making humanized antibodies are described, for example, in Winter, U.S. Pat. No. 5,225,539, Co et al., Nature 351, 501-502 (1992); Queen et al., Proc. Natl. Acad. Sci.

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86, 10029-1003 (1989) and Rodrigues et al., Int. J. Cancer, Supplement 7, 45-50 (1992).

75 Methods are also known for inducing expression of engineered antibodies in various cell types, such as mammalian and microbial cell types. Numerous techniques for preparing engineered antibodies are described, for example, in Owens and Young, "The genetic engineering of monoclonal antibodies," J. Immunol. Meth. 168, 149-165 (1994).

76 Methods for making single chain antibodies are also known in the art. Some suitable examples include those described by Wels et al. in European patent application 502 812 and Int. J. Cancer 60, 137-144 (1995).

77 Assays for directly detecting the presence of Y2H56 and its functional equivalents with antibodies follow known formats, such as, fluorescent activated flow cytometry, fluorescent microscopy, and immuno-electron microscopy. Moreover, assays for detecting the presence of proteins with antibodies have been previously described and follow known formats, such as standard blot and ELISA formats. These formats are normally based on incubating an antibody with a sample suspected of containing the protein and detecting the presence of a complex between the antibody and the protein. The antibody is labeled either before, during, or after the incubation step. The protein is preferably immobilized prior to detection. Immobilization may be accomplished by directly binding the protein to a solid surface, such as a microtiter well, or by binding the protein to immobilized antibodies.

78 Suitable assays are known in the art, such as the standard ELISA protocol described by R. H. Kenneth, "Enzyme-linked antibody assay with cells attached to polyvinyl chloride plates" in Kenneth et al., Monoclonal Antibodies, Plenum Press, New York, pp. 376 et seq. (1981).

DETAILED DESCRIPTION:

1 EXAMPLES

2 Example 1

3 Y2H56 Binds IKKs

4 A yeast two hybrid screen was undertaken with IKK.alpha. as a bait in an attempt to identify interacting proteins which could represent in vivo regulators of the cytokine induced kinase cascade. Full length IKK.alpha. and smaller fragments in the Field's pGTB9c bait vector (see Fields and Sternglanz, Trends Genet. 10, 286-292 (1994)) met with technical problems owing to its inherent in vivo transactivation properties. These problems were overcome by incorporating a high dose of an inhibitor of the product of the His3 selection gene thereby severely restricting yeast colony growth. (Triazole or 3-AT (3-amino-1, 2, 4-triazole or aminotriazole) has been reported to competitively inhibit the product of the yeast His3 gene in a dose dependent manner (Klopotowski et al., Arch. Biochem. Biophys. 112, 562-566 (1965)). The bait vector's insert was a 937 bp SnaB1/XhoI fragment of the murine IKK.alpha. clone encoding the protein's leucine zipper, helix-loop-helix and carboxyl terminus. The latter bait vector was transfected into the Y153 yeast strain and a colony that grew on agar without tryptophan was selected for further transfections according to standard protocols (Yeast Matchmaker manual, Clontech Inc., Palo Alto, Calif.). Yeast harboring the bait grew on histidine-minus plates. However, this non-specific growth was abrogated by the inclusion of 50 .mu.M (3-AT) that would also yield the strongest interactors. Y153 cells harboring the bait vector were transfected with a B lymphoblast cDNA library (0.6.times.10.sup.9 cfu, ATCC #87003) (Durfee et al., Genes Dev 7, 555-569 (1993)) sub-cloned into plasmid BNN132 (for a final transfection frequency

of 10.sup.5 clones), which were spread onto 30 agar plates (His-, Trp-, Leu-, 50 mM 3-AT). 126 clones showing a faster growth rate compared to background colonies were picked after 3 and 6 days incubtion at 30.degree. C. and replated. 70 clones were selected for plasmid isolation based on their growth on His-, Trp-, Leu-, 50 .mu.M 3-AT plates. From these 70 picks secondary picks, 16 clones remained positive after multiple rounds of purification and rescreening (14 of these sixteen were unique and two were isolated twice).

TABLE 1

Results of a Yeast Two-Hybrid Screen with IKK.alpha. Helix-Loop-Helix and Leucine Zipper Domains as Bait

Y2h Clones	Relative Interaction Strength	Insert Length	Identity
11	+	0.8 kB	RanBP5
52.sup.#	++	0.9 kB	CoA Reductase
21	++	1.3 kB	TRIP9/HuI.kappa.B.beta.2
29.sup.#	++	1.1 kB	HuTCP-1
31	++	1.5 kB	Hsp40
37	+	2.3 kB	BS4 (Interferon Induced Protein)
67	+	1.5 kB	Phospholipase A2
71	+	0.8 kB	Calmodulin
70	+	1.5 kB	HuSgn3
14*	++	1.2 kB	HuAD3 Locus
35*	+++	1.2 kB	Cosmid near Btk
56*	+++	0.9 kB	p33ING1-like
53*	+++	1.2 kB	Unknown
61**	+	0.7 kB	Unknown

Legend:
Fourteen yeast two hybrid clones obtained from a human B lymphoblastoid cell cDNA library which specifically interact with the contiguous helixloop-helix and leucine zipper domains of the IKK.alpha. protein. M clones (Y2h11,21,29, 70,14,35,56 and 53) also bound to an analogous IKK.beta. bait with similar or even greater strength except for Hsp40 which only specifically bound to the IKK.alpha. bait. All clones reproducibly failed to significantly interact with an empty bait vector and #two other bait vectors harboring either the IKK.alpha. Leucine Zipper or HelixLoop-Helix domains. The relative interaction strengths a: based on the growth rates (i.e., colony size) of each clone.
.sup.# Isolated Twice;
*Unknown strong interacting proteins;
**Unknown weak interacting protein.

The fourteen clones are shown in Table 1. These results demonstrate the presence of a family of IKK.alpha. binding proteins. Nine of the 14 clones are known proteins and the remaining five specify novel proteins: three of which interact with the bait more strongly than IKK.alpha.'s I.kappa.B.beta. substrate (Y2h35, 53 and 56), one in a comparable fashion to I.kappa.B.beta. (Y2h14) and one exhibited weaker binding (Y2h61). Several of the known proteins are involved in either signaling and/or molecular trafficking pathways in cells. RanBP5 was isolated as a Ran binding protein and Ran is a small GTP-binding and- hydrolyzing protein predominantly located in the nucleus (Deane et al., Mol. Cell Biol. 17, 5087-5096 (1998). RanBP5 is related to importin-.beta., a mediator of nuclear localization signal (NLS)-dependent nuclear transport. TRIP9/HuI.kappa.B.beta.2 is the predominant isoform of I.kappa.B.beta. in human cells and a known physiological substrate of the IKK.alpha. kinase (Lee et al., Mol.

Endocrinol. 9, 243-254 (1995); Hirano et al., Mol. Cell. Biol. 18, 2596-2607 (1998)). The presence of I.kappa.B.beta. amongst these IKK.alpha. interacting proteins validates the specificity of the screen and also demonstrates the I.kappa.Bs do not require the IKK.alpha. amino terminal kinase domain for binding. Hsp40 and TCP-1 are chaperone proteins which might bind to the bait due to a partially unfolded conformation (in the context of a Gal4dbd chimera). A database of frequently isolated clones in yeast two hybrid screens does contain several hsp proteins but Hsp40 and TCP1 are not represented amongst these frequently isolated, presumably false positive genes. Alternatively, they may also be natural interactors of IKK.alpha. that might be involved in its in vivo cytoplasmic trafficking. HuSgn3 was recently described as a component of a 450 kDa protein complex that also possesses an I.kappa.B kinase activity. Seeger et al., FASEB J. 12, 469-478 (1998). Sgn3 also exhibited sequence similarities to regulatory components of the 26S proteasome complex. Calmodulin is the principal calcium sensor in the cell, which when complexed to two calcium ions, acts as a regulator for a variety of intracellular enzymes including kinases such as CaM-kinase II, the serine/threonine specific phosphatase, Calcineurin and proteins which maintain the cytoskeletal architecture.

6 Y2H56 is highly homologous with the p33-ING1 tumor suppressor protein having about 45% identity and about 70% overall similarity. The p33-ING1 tumor suppressor protein has been shown to functionally interact with the p53 tumor suppressor protein to arrest cellular growth and induce apoptosis. Garkavtsev et al., Nature Genetics 14, 415-420 (1996).

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CLAIMS:

What is claimed is:

1. An isolated nucleic acid molecule comprising a sequence that encodes an IKK binding protein having SEQ ID NO:1 or its allelic variants.

2. An isolated nucleic acid molecule according to claim 1 comprising SEQ ID NO:2, SEQ ID NO:3, or sequences that have at least 85% identity thereto.

3. An isolated nucleic acid molecule according to claim 1 comprising SEQ ID NO:2 or SEQ ID NO:3.

4. An isolated nucleic acid molecule encoding an IKK binding protein that hybridizes under stringent conditions to a nucleic acid molecule selected from the group consisting of SEQ ID NO:2, and SEQ ID NO:3.

5. An isolated nucleic acid molecule fully complementary to the nucleic acid molecule of either SEQ ID NO:2 or SEQ ID NO:3.

6. A method of making an IKK binding protein or its allelic variants, comprising:

incorporating into a host cell a nucleic acid molecule that encodes an IKK binding protein comprising a sequence as set forth as SEQ ID NO:1 or its allelic variants;

expressing the nucleic acid molecule; and

isolating the IKK binding protein or its allelic variants.

7. A method according to claim 6, wherein the nucleic acid molecule that encodes an IKK binding protein comprising a sequence set forth as SEQ ID NO:1 or its allelic variants comprises either SEQ ID NO:2 or SEQ ID NO:3.

8. A method of making an IKK binding protein, comprising:

incorporating into a host cell a nucleic acid molecule that encodes an IKK binding protein wherein the nucleic acid molecule that encodes an IKK binding protein or its allelic variants comprises a nucleic acid molecule that is at least 85% identical to either the nucleic acid molecule of SEQ ID NO:2 or SEQ ID NO:3.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Db    780 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAACTACCCTT 839

Qy    936 GTTCGGTTGATACTTAGTAAC 956
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Db    840 GTTCGGNTGATACTTAGTAAC 860


RESULT 2
BQ679158
LOCUS       BQ679158                995 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8034407 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6213872
            5', mRNA sequence.
ACCESSION   BQ679158
VERSION     BQ679158.1  GI:21791837
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 995)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2380  row: e  column: 09
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .995
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6213872"
                     /clone_lib="NIH_MGC_112"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      268 a    260 c    287 g    180 t
ORIGIN

  Query Match           77.8%;  Score 745;  DB 14;  Length 995;
  Best Local Similarity   98.0%;  Pred. No. 8.6e-179;
  Matches  765;  Conservative    0;  Mismatches   15;  Indels    1;  Gaps    1;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    106 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 165

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    286 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 345

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    346 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 405

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 525

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 585

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    586 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 645

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
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Db    646 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 705

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTG-CCCGGATCCGAGG 874
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Db    706 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCCGGATCCGAGG 765

Qy    875 AGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCT 934
            || ||||||||||||||| ||||||||||||||||||||  | ||| ||||||||
Db    766 GAGCAGGTAATCTGTCCCTTCTTTCGTGTCGCAATATTTCCCTGTCCTTTTAAACTACCC 825

Qy    935 T 935
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Db    826 T 826
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RESULT 3
BQ686855
LOCUS       BQ686855                904 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8343972 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6248487
            5', mRNA sequence.
ACCESSION   BQ686855
VERSION     BQ686855.1  GI:21812171
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2388  row: g  column: 16
            High quality sequence stop: 664.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6248487"
                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      252 a    215 c    265 g    170 t      2 others
ORIGIN
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  Query Match             76.8%;  Score 735.8;  DB 14;  Length 904;
  Best Local Similarity   97.8%;  Pred. No. 1.9e-176;
  Matches  787;  Conservative    0;  Mismatches   14;  Indels    4;  Gaps    4;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     60 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 119

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    120 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 179

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    180 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 239

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    240 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 299

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    300 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 359

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    360 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 419

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    420 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 479

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    480 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 539

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 599

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    600 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 659

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
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Db    660 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGNTCTGTCCA 719

Qy    816 CGGTGTGT-CCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCC-GGATCCGAG 873
          |||||||| ||||| |||||||||||||||| |||||||||||||||| |||||||||||
Db    720 CGGTGTGTCCCAGGNAAAGAGGAAGAAGAAGTAAGAGGAGCTGTGTGCCCGGGATCCGAG 779

Qy    874 GAGCAAGTTAATCTGT-CCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTAC 932
          |||||||||||||||| |||||| |||||||||||||||||||| | | ||||||||||||
Db    780 GAGCAAGTTAATCTGTCCCCTTCTTTCGTGTCGCAATATTTCCCCTTCCTTTAAAACTAC 839

Qy    933 CTTGTTC-GGTTGATACTTAGTAAC 956
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Db    840 CTTGGTCGGGTTGATACTTAAAAAC 864
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RESULT 4
BQ687622
LOCUS       BQ687622                879 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8171406 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6251931
            5', mRNA sequence.
ACCESSION   BQ687622
VERSION     BQ687622.1  GI:21812938
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 879)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2397  row: g  column: 04
            High quality sequence stop: 645.
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                     /clone_lib="NIH_MGC_110"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      245 a    210 c    256 g    168 t
ORIGIN

  Query Match             75.5%;  Score 723;  DB 14;  Length 879;
  Best Local Similarity   98.2%;  Pred. No. 3.3e-173;
  Matches  773;  Conservative    0;  Mismatches   10;  Indels    4;  Gaps    4;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     40 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 99

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 159

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 219

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    220 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 279

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    280 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 339

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    340 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 399

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    400 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 459

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 519

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    520 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 579

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    580 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 639

Qy    756 TGGTTTCACTTTGCCTGCGT-GGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCC 814
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Db    640 TGGTTTCACTTTGCCTGCGTGGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCC 699

Qy    815 ACGGTGTGTCCAGGAAAAGA-GGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGA- 872
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Db    700 ACGGTGTGTCCAGGAAAAGAGGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCCGATCCGAG 759

Qy    873 GGAGCAAGTTAATCTGTCCC-TTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTA 931
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Db    760 GGAGCAAGTTAATCTGTCCCTTTCTTTCGTGTCGCAATATTTCCCCTTCCTTTAAAACTA 819

Qy    932 CCTTGTT 938
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Db    820 CCTTGGT 826


RESULT 5
BQ877416
LOCUS       BQ877416                941 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8071188 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6090578
            5', mRNA sequence.
ACCESSION   BQ877416
VERSION     BQ877416.1  GI:22269424
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2332  row: d  column: 03
            High quality sequence stop: 656.
FEATURES             Location/Qualifiers
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                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
```

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 262 a 238 c 266 g 175 t
ORIGIN

Query Match 74.6%; Score 714.6; DB 14; Length 941;
Best Local Similarity 98.3%; Pred. No. 4.6e-171;
Matches 764; Conservative 0; Mismatches 9; Indels 4; Gaps 4;

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Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    106 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 165

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    286 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 345

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    346 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 405

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Db    466 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 525

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    526 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 585

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    586 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 645

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
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Db    646 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 705

Qy    816 CGGTGTGTCCAGG-AAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTG-CCCGGATCCGAG 873
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Db    706 CGGTGTGTCCAGGCAAAAGAGGAAGAAGAAATAGGAGGAGCTGTGTGCCCCGGATCCGAG 765

Qy    874 GAGCAAGTTAATCT-GTCCCTTCATTCGT-GTCGCAATATTTCCCTTCCTTTTAAAA 928
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Db    766 GAGCAAGTTAATCTGGTCCCTTCATTCGTGGTCCCAATATTTCCCTTTCCTTTTAAA 822
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RESULT 6
BQ883988
LOCUS BQ883988 989 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT_8073788 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6083492 5', mRNA sequence.
ACCESSION BQ883988
VERSION BQ883988.1 GI:22275996
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 989)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2313 row: l column: 21
High quality sequence start: 21
High quality sequence stop: 589.
FEATURES Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 260 a 257 c 288 g 184 t
ORIGIN

Query Match 74.2%; Score 711; DB 14; Length 989;
Best Local Similarity 95.3%; Pred. No. 3.8e-170;
Matches 765; Conservative 0; Mismatches 35; Indels 3; Gaps 3;

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Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     69 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 128

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    129 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 188

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    189 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 248

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    249 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 308

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Db    309 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 368

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    429 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 488

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Db    489 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 548
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Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    549 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCCAACGAACCCACGTACTGCCTG 608

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Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
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Db    669 TGGTTTCCCTTTGCCTGCGTGGACCTTTACACAAAACCC-AAGGAAAATGGTTCTGTCCA 727

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTA-GGAGGAGCTGTGTG-CCCGGATCCGAG 873
          | | ||| || |||||||||||||||||||||| |||||||||||||| |||||| |||||
Db    728 CCGGGTGGCCCGGAAAAGAGGAAGAAGAAGTAGGGAGGAGCTGTGTGCCCCGGACCCGAG 787

Qy    874 GAGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACC 933
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Db    788 GAGCAGGTTAATCTGGCCCCTTCTTTCCGGCCGCAATATTTCCCTTCTTTTTAAACTACC 847

Qy    934 TTGTTCGGTTGATACTTAGTAAC 956
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Db    848 TTGGTCGGGTGATACTTAGTAAC 870


RESULT 7
BQ688356
LOCUS       BQ688356                874 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8064337 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6207958
            5', mRNA sequence.
ACCESSION   BQ688356
VERSION     BQ688356.1  GI:21813672
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 874)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2364  row: n  column: 23
            High quality sequence stop: 649.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed  by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of  California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      246 a    209 c    255 g    164 t
ORIGIN

  Query Match             72.1%;  Score 690.6;  DB 14;  Length 874;
  Best Local Similarity   97.1%;  Pred. No. 5.8e-165;
  Matches  768;  Conservative    0;  Mismatches   14;  Indels    9;  Gaps    6;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     40 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 99

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    100 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 159

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    160 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 219

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    280 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 339

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    340 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 399

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Db    400 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 459

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    520 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 579

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    580 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 639

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCC-AAAGGAAAATGGTTCTGTCC 814
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Db    640 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAAGGAAAATGGGTCTGTCC 699

Qy    815 ACGGTGTGTCCAGGAAAAGA-GGAAGAAGAAGTAGGAGGAGCTGTGTG-CCCGGATCCGA 872
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Db    700 ACGGTGTGTCCAGGAAAAGAGGGAAGAAAAAGTAGGAGGAGCTGTGTGCCCCGGATCCGA 759

Qy    873 GGAGCAA-GTTAATCTGT-CCCTTCATTCGTGTCGCAA----TATTTCCCTTCCTTTTAA 926
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Db    760 GGAGCAAGGTTAATCTGTCCCCTTCATTCGTGTCGCAAATATTTTCCCCTTCCCTTTTAA 819

Qy    927 AACTACCTTGT 937
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Db    820 AACTAACCTTT 830


RESULT 8
BQ683118
LOCUS       BQ683118                905 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8208770 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6260378
            5', mRNA sequence.
ACCESSION   BQ683118
VERSION     BQ683118.1  GI:21795797
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 905)
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  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2419  row: g  column: 03
            High quality sequence stop: 653.
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                     /clone_lib="NIH_MGC_112"
                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      249 a    230 c    266 g    160 t
ORIGIN

  Query Match             71.5%;  Score 685.2;  DB 14;  Length 905;
  Best Local Similarity   98.7%;  Pred. No. 1.4e-163;
  Matches  701;  Conservative    0;  Mismatches    8;  Indels    1;  Gaps    1;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    106 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 165

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    586 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 645

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
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Db    646 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 705

Qy    816 CGGTGTGTCCA-GGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCC 864
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Db    706 CGGTGTGTCCAGGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGGGGTGCC 755


RESULT 9
BG753113
LOCUS       BG753113                719 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602732385F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4875764 5',
            mRNA sequence.
ACCESSION   BG753113
VERSION     BG753113.1  GI:14063766
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 719)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1757  row: j  column: 21
            High quality sequence stop: 713.
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                     /clone_lib="NIH_MGC_43"
                     /tissue_type="normal pigmented retinal epithelium"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT      212 a    171 c    213 g    123 t
ORIGIN

  Query Match             69.9%;  Score 669.4;  DB 12;  Length 719;
  Best Local Similarity   99.0%;  Pred. No. 1.4e-159;
  Matches  684;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    149 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 208

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    209 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 268

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    269 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 328

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    329 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 388

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    389 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 448

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    449 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 508

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    509 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 568

Qy    696 TGCCACCAGGTCTCCTATGGG-GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGA 754
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Db    569 TGCCACCAGGTCTCCTATGGGCGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGA 628

Qy    755 GTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCC 814
          ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db    629 GTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAATACCAAAGGAAAATGGTTCTGTCC 688

Qy    815 ACGGTGTGTCCAGGAAAAGAGGAAGAAGAAG 845
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Db    689 ACGGTGTGTCCAGGAAAAGAGGAAGAAGAAG 719


RESULT 10
BQ678481
LOCUS       BQ678481                952 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8208766 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6260282
            5', mRNA sequence.
ACCESSION   BQ678481
VERSION     BQ678481.1  GI:21791160
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 952)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2419  row: c  column: 03
            High quality sequence stop: 592.
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                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      234 a    297 c    257 g    163 t      1 others
ORIGIN

  Query Match             68.2%;  Score 653.6;  DB 14;  Length 952;
  Best Local Similarity   95.8%;  Pred. No. 1.5e-155;
  Matches  682;  Conservative    0;  Mismatches   29;  Indels    1;  Gaps    1;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
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Db    346 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 405

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    466 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 525

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    526 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 585

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          |||||||||||||||||||||||||||||||||||| |||||||||||||| | |||
Db    586 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACCATCCAGACTGTCCATTCGAG 645

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          ||||||| |||||||||||||||||||| |||||||||||||| | || |||||||
Db    646 TGGTTTCCCTTTGCCTGCGTGGACCTTACCCCGAAACCCAAAGGAACACGGGTCTGTCCC 705

Qy    816 CGGTGTGTCCAGGA-AAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGG 866
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Db    706 CGCTGGGCCCCGCACCAAAAGGAAAACAAGCCAGGAGGACCCGTGTCCCCGG 757


RESULT 11
BG749339
LOCUS       BG749339                720 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602707806F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844664 5',
            mRNA sequence.
ACCESSION   BG749339
VERSION     BG749339.1  GI:14059992
KEYWORDS    EST.
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SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1682  row: k  column: 01
            High quality sequence stop: 713.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and  Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library. |"
BASE COUNT     209 a    177 c    212 g    122 t
ORIGIN

  Query Match             67.1%;  Score 642.8;  DB 12;  Length 720;
  Best Local Similarity   98.4%;  Pred. No. 8.1e-153;
  Matches  681;  Conservative    0;  Mismatches    7;  Indels    4;  Gaps    3;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     29 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 88

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 148

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    149 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 208

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    209 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 268

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    269 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 328

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 388

Qy    516 GGCCGGGGTCAG--AAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGG 573
          ||||||||||||   | ||||||||||||||||||||||||||||||||||||||||||
Db    389 GGCCGGGGTCAGCACACGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGG 448

Qy    574 AAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGT 633
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Db    449 AAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGT 508

Qy    634 CCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCC 693
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Db    509 CCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCC 568

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Qy    754 AGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGA-AAATGGTTCTGT 812
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Db    629 AGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGACACATGGTTCTGT 688

Qy    813 CCACGGTGTGTCCAGGAA-AAGAGGAAGAAGA 843
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Db    689 CCACGGTGTGTCCAGGAACAAGAGGAAGAAGA 720


RESULT 12
BQ675901
LOCUS       BQ675901                951 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8297255 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6274178
            5', mRNA sequence.
ACCESSION   BQ675901
VERSION     BQ675901.1  GI:21788593
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 951)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2455  row: f  column: 03
            High quality sequence stop: 574.
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                     /tissue_type="melanotic melanoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      249 a    243 c    304 g    155 t
ORIGIN

  Query Match             66.4%;  Score 635.8;  DB 14;  Length 951;
  Best Local Similarity   93.6%;  Pred. No. 5.1e-151;
  Matches  697;  Conservative    0;  Mismatches   42;  Indels    6;  Gaps    3;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    106 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 165

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
Db    286 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 345

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
Db    346 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 405

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
Db    466 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 525

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
Db    526 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 585

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
Db    586 TGCCACCAGGTCTCCTATGGGGAGATGATTGGGTGTGACCATCCAAACTGTCCCATTGAG 645

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGT--- 812
Db    646 TGGGTTCCCTTTGCCTGGGGGGACCTTACCCCCAAACCCCAAGGAAAATGGGTTCTTGCC 705

Qy    813 CCACGGTGTGTCCAGGAAAAGAGGAAGAAGAAG-TAGGAGGAGCTGTGTG--CCCGGATC 869
Db    706 CCGGGGGGGTCCCGGGAAAAAAGGAGGAGGAAGTTAGGAGGGGCTGGGCGGCCCGGGATC 765

Qy    870 CGAGGAGCAAGTTAATCTGTCCCTT 894
Db    766 CGAGGAGCCAAGTGATGGGGGCCCT 790


RESULT 13
BQ677883
LOCUS       BQ677883                913 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8183997 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6264048
            5', mRNA sequence.
ACCESSION   BQ677883
VERSION     BQ677883.1  GI:21790562
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 913)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

            Plate: LLCM2428  row: p  column: 01
            High quality sequence stop: 607.
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                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      238 a    251 c    293 g    131 t
ORIGIN

  Query Match             64.0%;  Score 613.2;  DB 14;  Length 913;
  Best Local Similarity   93.9%;  Pred. No. 2.8e-145;
  Matches  661;  Conservative    0;  Mismatches   38;  Indels    5;  Gaps    2;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
Db     46 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 105

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
Db    106 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 165

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
Db    166 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 225

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
Db    226 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 285

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
Db    286 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 345

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
Db    346 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 405

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
Db    406 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 465

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
Db    466 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 525

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
Db    526 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 585

Qy    696 TGCCACCAGGTCTCCTATGGGGAGA---TGATTGGCTGTGACAATCCAGACTGTCCAATT 752
Db    586 TGCCACCAGGTCTCCCTATGGGGGAGATGATTGGGCTGTGACAATCCAGACTGTCCAATT 645

Qy    753 GAGTGGTTTCACTTT--GCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCT 810
Db    646 GAGTGGGTTCCCTTTTGCCTGCGGGGGACCTTACCACGAAACCCAAGGGAAAATGGTCCT 705

Qy    811 GTCCACGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAG 854
Db    706 GTCCACGGGGGGTCCCCCAAACGCCCGCAAAGAACGAGCAGGAG 749
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RESULT 14
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LOCUS       BQ682571                911 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8212749 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6272913
            5', mRNA sequence.
ACCESSION   BQ682571
VERSION     BQ682571.1  GI:21795250
KEYWORDS    EST.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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                     NIH_MGC Library."
BASE COUNT      229 a    227 c    326 g    128 t      1 others
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REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
  PUBMED    10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
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REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1871)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
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            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of subtraction to Rot = 20.0. Second strand cDNA
            was prepared with the primer adapter of sequence[5'
            GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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85: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	958	100.0	958	18	US-09-442-013-7	Sequence 7, Appli
2	936.4	97.7	1300	30	US-09-799-451-403	Sequence 403, App
3	798.4	83.3	1108	18	US-09-442-013-1	Sequence 1, Appli
4	794.6	82.9	1073	28	US-09-716-972-4875	Sequence 4875, Ap
5	794.6	82.9	1073	29	US-09-721-588-5351	Sequence 5351, Ap
6	794.6	82.9	2537	69	US-60-250-830-3236	Sequence 3236, Ap
7	794.6	82.9	2537	76	US-60-323-966-3236	Sequence 3236, Ap
8	787.4	82.2	807	18	US-09-442-013-3	Sequence 3, Appli
9	787.4	82.2	807	18	US-09-442-013-5	Sequence 5, Appli
10	771	80.5	1082	1	PCT-US02-25465-43	Sequence 43, Appl
11	647.4	67.6	958	18	US-09-442-013-9	Sequence 9, Appli
12	645.6	67.4	1275	62	US-60-184-797-652	Sequence 652, App
13	645.6	67.4	1275	71	US-60-278-258-16936	Sequence 16936, A
14	641.8	67.0	1465	1	PCT-US01-04098A-646	Sequence 646, App
15	641.8	67.0	1465	24	US-09-620-325-298	Sequence 298, App
16	622	64.9	1011	20	US-09-532-645-18	Sequence 18, Appl
17	622	64.9	1011	56	US-60-126-246-5	Sequence 5, Appli
18	449.4	46.9	1199	1	PCT-US01-03800A-924	Sequence 924, App
19	449.4	46.9	1199	1	PCT-US01-04098A-2614	Sequence 2614, Ap
20	449.4	46.9	1199	18	US-09-496-914A-7985	Sequence 7985, Ap
21	449.4	46.9	1199	22	US-09-560-875A-7985	Sequence 7985, Ap

	22	438.4	45.8	974	62	US-60-184-797-1099 Sequence 1099, Ap
	23	434	45.3	466	25	US-09-649-164-5599 Sequence 5599, Ap
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c	25	427.6	44.6	693	18	US-09-496-914A-5424 Sequence 5424, Ap
c	26	427.6	44.6	693	22	US-09-560-875A-5424 Sequence 5424, Ap
	27	378	39.5	432	29	US-09-721-588-3653 Sequence 3653, Ap
	28	376.6	39.3	456	16	US-09-234-611-9815 Sequence 9815, Ap
	29	376.6	39.3	456	16	US-09-235-076-16047 Sequence 16047, A
	30	376.6	39.3	456	16	US-09-248-797-32620 Sequence 32620, A
	31	376.6	39.3	456	17	US-09-332-782-16047 Sequence 16047, A
	32	376.6	39.3	456	29	US-09-737-223-16047 Sequence 16047, A
	33	376.6	39.3	456	34	US-09-904-809-9815 Sequence 9815, Ap
	34	376.6	39.3	456	34	US-09-918-995-16047 Sequence 16047, A
	35	376.6	39.3	456	34	US-09-925-564-32620 Sequence 32620, A
	36	361.2	37.7	443	29	US-09-758-472-2828 Sequence 2828, Ap
	37	361.2	37.7	443	42	US-10-235-926-2828 Sequence 2828, Ap
	38	351.6	36.7	428	18	US-09-496-911-13363 Sequence 13363, A
	39	351.6	36.7	428	36	US-09-975-673A-13363 Sequence 13363, A
	40	351.6	36.7	435	18	US-09-496-911-13364 Sequence 13364, A
	41	351.6	36.7	435	36	US-09-975-673A-13364 Sequence 13364, A
	42	346	36.1	402	17	US-09-362-510-4047 Sequence 4047, Ap
	43	346	36.1	402	17	US-09-362-510A-4047 Sequence 4047, Ap
	44	346	36.1	402	34	US-09-904-013-4047 Sequence 4047, Ap
	45	325.2	33.9	359	28	US-09-716-972-2963 Sequence 2963, Ap

ALIGNMENTS

RESULT 1
US-09-442-013-7
; Sequence 7, Application US/09442013
; GENERAL INFORMATION:
; APPLICANT: Lou, Ying
; APPLICANT: Xu, Xiang
; APPLICANT: Leo, Cindy
; APPLICANT: Huang, Betty
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: A-68289/DJB/RMS/DAV
; CURRENT APPLICATION NUMBER: US/09/442,013
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-442-013-7

Query Match 100.0%; Score 958; DB 18; Length 958;
Best Local Similarity 100.0%; Pred. No. 3.3e-247;
Matches 958; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 TTTGCTGACCTCAGCCCTGCGTGGGCGTATTGAGGGTCTGCGTGGCTGAGCATCCAGTGT 60

Qy      61 CCTTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAA 120
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Db      61 CCTTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAA 120

Qy     121 TGGGAGCAAGAGTCACTCCACGAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCT 180
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Qy     181 GCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGA 240
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Qy     361 GTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAA 420
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Db     361 GTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAA 420

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Qy     661 TGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGA 720
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Db     661 TGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGA 720

Qy     721 TGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACC 780
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Db     721 TGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACC 780

Qy     781 TTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGGAAGA 840
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Db     781 TTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGGAAGA 840

Qy     841 AGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGAGCAAGTTAATCTGTCCCTTCATTCG 900
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Db     841 AGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGAGCAAGTTAATCTGTCCCTTCATTCG 900

Qy     901 TGTCGCAATATTTCCCTTCCTTTTAAAACTACCTTGTTCGGTTGATACTTAGTAACAA 958
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RESULT 2
US-09-799-451-403
; Sequence 403, Application US/09799451
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451

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;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 948
;  SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 403
;   LENGTH: 1300
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (188)..(913)
US-09-799-451-403

  Query Match             97.7%;  Score 936.4;  DB 30;  Length 1300;
  Best Local Similarity   98.8%;  Pred. No. 2.5e-241;
  Matches  943;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      3 TGCTGACCTCAGCCCTGCGTGGGCGTATTGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 62
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Db     71 TGCTGACCTCAGCCCTGGCGTGGGCATAGGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 130

Qy     63 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 122
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Db    131 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 190

Qy    123 GGAGCAAGAGTCACTCCACGAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 182
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Db    191 GGAGCAAGAGTCACTCCACAAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 250

Qy    183 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 242
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Db    251 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 310

Qy    243 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGAC 302
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Qy    303 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 362
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Db    371 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 430

Qy    363 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 490

Qy    423 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 482
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Db    491 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 550

Qy    483 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 542
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Db    551 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 610

Qy    543 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 602
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Db    611 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 670

Qy    603 GGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCTGATGTGCTGGACATG 662
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Qy    663 CCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATG 722
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Qy    723 ATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTT 782
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Qy    783 ACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGGAAGAAG 842
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Qy    843 AAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGAGCAAGTTAATCTGTCCCTTCATTCGTG 902
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Db    971 TCGCAATATTTCCCTTCCTTTTAAAACTACCTTGTTCGGTTGATACTTAGTAAC 1024


RESULT 3
US-09-442-013-1
; Sequence 1, Application US/09442013
; GENERAL INFORMATION:
;  APPLICANT:  Lou, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Huang, Betty
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION:  NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE:  A-68289/DJB/RMS/DAV
;  CURRENT APPLICATION NUMBER: US/09/442,013
;  CURRENT FILING DATE:  1999-11-17
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1108
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-442-013-1

  Query Match             83.3%;  Score 798.4;  DB 18;  Length 1108;
  Best Local Similarity   99.3%;  Pred. No. 3.8e-204;
  Matches  802;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    149 TGGAGGCCTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGAT 208
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Db    301 TGCTGGGATTACAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGAT 360

Qy    209 GCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGA 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGA 420

Qy    269 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT 480

Qy    329 CCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCA 388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCA 540

Qy    389 GACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGA 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGA 600

Qy    449 AGCAGATCTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTT 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAGATCTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTT 660

Qy    509 AAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATC 720

Qy    569 AGAGGAAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCAT 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGAGGAAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCAT 780

Qy    629 CCTGTCCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTA 688
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Db    781 CCTGTCCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTA 840

Qy    689 CTGCCTGTGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCC 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTGCCTGTGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCC 900
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Qy    749 AATTGAGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTT 808
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Db    901 AATTGAGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTT 960

Qy    809 CTGTCCACGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGAT 868
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Db    961 CTGTCCACGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGAT 1020

Qy    869 CCGAGGAGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAA 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCGAGGAGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAA 1080

Qy    929 CTACCTTGTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||||||||
Db   1081 CTACCTTGTTCGGTTGATACTTAGTAAC 1108
```

RESULT 4
US-09-716-972-4875
; Sequence 4875, Application US/09716972
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Vasicek, Thomas
; APPLICANT: Lee, John
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2030-001
; CURRENT APPLICATION NUMBER: US/09/716,972
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/166,948
; PRIOR FILING DATE: 1999-11-22
; NUMBER OF SEQ ID NOS: 5251
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4875
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-716-972-4875

Query Match 82.9%; Score 794.6; DB 28; Length 1073;
Best Local Similarity 99.5%; Pred. No. 4e-203;
Matches 797; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 97

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 157

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 217

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 277

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 337

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 397

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 457

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 517

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 577

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 637

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 697

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 757

Qy    876 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 817

Qy    936 GTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||
Db    818 GTTCGGTTGATACTTAGTAAC 838
```

RESULT 5
US-09-721-588-5351
; Sequence 5351, Application US/09721588
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Villeval, Jean-Luc
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2046-001
; CURRENT APPLICATION NUMBER: US/09/721,588
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 60/167,381
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 5410
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5351
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-721-588-5351

Query Match 82.9%; Score 794.6; DB 29; Length 1073;
Best Local Similarity 99.5%; Pred. No. 4e-203;
Matches 797; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 97

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 157

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 217

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 277

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    278 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 337

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 397

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 457

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 517

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 577

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 637

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 697

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 757

Qy    876 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 817

Qy    936 GTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||
Db    818 GTTCGGTTGATACTTAGTAAC 838


RESULT 6
US-60-250-830-3236
; Sequence 3236, Application US/60250830
; GENERAL INFORMATION:
;  APPLICANT:  Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION:  METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE:  GX-0020 P
;  CURRENT APPLICATION NUMBER: US/60/250,830
;  CURRENT FILING DATE:  2000-11-04
;  NUMBER OF SEQ ID NOS:  3246
;  SOFTWARE:  PERL Program
; SEQ ID NO 3236
;   LENGTH: 2537
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 121128.18
US-60-250-830-3236

  Query Match            82.9%;  Score 794.6;  DB 69;  Length 2537;
  Best Local Similarity  99.5%;  Pred. No. 5.3e-203;
  Matches  797;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 115

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 175

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 235

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 295

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 355

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 415

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 475

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    476 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 535

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 595

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    596 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 655

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    656 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 715

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 875
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    716 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 775

Qy    876 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    776 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 835

Qy    936 GTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||
Db    836 GTTCGGTTGATACTTAGTAAC 856


RESULT 7
US-60-323-966-3236
; Sequence 3236, Application US/60323966
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0020-1 P
;  CURRENT APPLICATION NUMBER: US/60/323,966
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 3246
;  SOFTWARE: PERL Program
; SEQ ID NO 3236
;   LENGTH: 2537
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 121128.18
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US-60-323-966-3236

  Query Match             82.9%;  Score 794.6;  DB 76;  Length 2537;
  Best Local Similarity   99.5%;  Pred. No. 5.3e-203;
  Matches  797;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 115

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 175

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 235

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 295

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 355

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 415

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 475

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    476 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 535

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 595

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    596 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 655

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    656 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 715

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 875
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    716 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGA 775

Qy    876 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    776 GCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTT 835

Qy    936 GTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||
Db    836 GTTCGGTTGATACTTAGTAAC 856


RESULT 8
US-09-442-013-3
; Sequence 3, Application US/09442013
; GENERAL INFORMATION:
;  APPLICANT:  Lou, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Huang, Betty
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION:  NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE:  A-68289/DJB/RMS/DAV
;  CURRENT APPLICATION NUMBER: US/09/442,013
;  CURRENT FILING DATE:  1999-11-17
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-442-013-3

  Query Match             82.2%;  Score 787.4;  DB 18;  Length 807;
  Best Local Similarity   98.6%;  Pred. No. 3.2e-201;
  Matches  794;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      3 TGCTGACCTCAGCCCTGCGTGGGCGTATTGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 62
          |||||||||||||||||    ||       ||||||||||||||||||||||||||||||
Db      1 TGCTGACCTCAGCCCTGGCGTGGGCATAGGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 60

Qy     63 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 120

Qy    123 GGAGCAAGAGTCACTCCACGAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 182
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGCAAGAGTCACTCCACAAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 180

Qy    183 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 240

Qy    243 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGAC 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGAC 300

Qy    303 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 360

Qy    363 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 420

Qy    423 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 480

Qy    483 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 540

Qy    543 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 600

Qy    603 GGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCTGATGTGCTGGACATG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCTGATGTGCTGGACATG 660

Qy    663 CCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATG 720

Qy    723 ATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTT 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTT 780

Qy    783 ACCACGAAACCCAAAGGAAAATGGT 807
          |||||||||||||||||||||||||
Db    781 ACCACGAAACCCAAAGGAAAATGGT 805
```

```
RESULT 9
US-09-442-013-5
; Sequence 5, Application US/09442013
; GENERAL INFORMATION:
;  APPLICANT:  Lou, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Huang, Betty
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION:  NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE:  A-68289/DJB/RMS/DAV
;  CURRENT APPLICATION NUMBER: US/09/442,013
;  CURRENT FILING DATE:  1999-11-17
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 807
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-442-013-5

  Query Match             82.2%;  Score 787.4;  DB 18;  Length 807;
  Best Local Similarity   98.6%;  Pred. No. 3.2e-201;
  Matches  794;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      3 TGCTGACCTCAGCCCTGCGTGGGCGTATTGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 62
          ||||||||||||||||||    ||      ||||||||||||||||||||||||||||||
Db      1 TGCTGACCTCAGCCCTGGCGTGGGCATAGGAGGGTCTGCGTGGCTGAGCATCCAGTGTCC 60

Qy     63 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TTCGTACTGCCACTGACAGCCTCAGGCCTGATTTCCAGCACTGTCTGTCCAGGAGCAATG 120

Qy    123 GGAGCAAGAGTCACTCCACGAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 182
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    121 GGAGCAAGAGTCACTCCACAAGACTCTGGAGGCCTGATAGGTATCGAGAACCTTCCCTGC 180

Qy    183 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAA 240

Qy    243 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGAC 302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGAC 300

Qy    303 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGT 360

Qy    363 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGG 420

Qy    423 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGAT 480

Qy    483 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGG 540

Qy    543 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAA 600

Qy    603 GGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCTGATGTGCTGGACATG 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCTGATGTGCTGGACATG 660

Qy    663 CCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATG 720

Qy    723 ATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTT 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTT 780

Qy    783 ACCACGAAACCCAAAGGAAAATGGT 807
          |||||||||||||||||||||||||
Db    781 ACCACGAAACCCAAAGGAAAATGGT 805


RESULT 10
PCT-US02-25465-43
; Sequence 43, Application PC/TUS0225465
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  BARROSO, Ines
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  DUGGAN, Brendan M.
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  FORSYTHE, Ian J.
;  APPLICANT:  GIETZEN, Kimberly J.
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  GRAUL, Richard C.
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  GURURAJAN, Rajagopal
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  ISON, Craig H.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  LEE, Sally
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  LI, Joana X.
;  APPLICANT:  REDDY, Roopa
;  APPLICANT:  RICHARDON, Thomas W.
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  WARREN, Bridget A.
;  APPLICANT:  XU, Yuming
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  YUE, Huibin
;  TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEA
;  FILE REFERENCE: PF-1126 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/25465
;  CURRENT FILING DATE:  2002-08-08
;  PRIOR APPLICATION NUMBER: US 60/311,017
;  PRIOR FILING DATE: 2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/313,070
;  PRIOR FILING DATE: 2001-08-17
;  PRIOR APPLICATION NUMBER: US 60/313,071
;  PRIOR FILING DATE: 2001-08-17
;  PRIOR APPLICATION NUMBER: US 60/314,678
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/316,692
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 60/317,913
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US 60/322,182
;  PRIOR FILING DATE: 2001-09-14
;  PRIOR APPLICATION NUMBER: US 60/340,747
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/342,761
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: US 60/369,129
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PERL Program
; SEQ ID NO 43
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;   LENGTH: 1082
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 72332548CB1
PCT-US02-25465-43

  Query Match             80.5%;  Score 771;  DB 1;  Length 1082;
  Best Local Similarity   99.1%;  Pred. No. 9.3e-197;
  Matches  796;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     43 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 102

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    103 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 162

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    163 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 222

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    223 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 282

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    283 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 342

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 402

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 462

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    463 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGCCC 522

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 582

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 642

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 815
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCA 702

Qy    816 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGC-TGTGTGCCC-GGATCCGAG 873
          |||||||||||||||||||||||||||||||||||| |||||||| |||||||| |||||||
Db    703 CGGTGTGTCCAGGAAAAGAGGAAGAAGAAGTAGGAGGAGCATGTGTGCCCAGGATCCGAG 762

Qy    874 GAGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACC 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 GAGCAAGTTAATCTGTCCCTTCATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACC 822

Qy    934 TTGTTCGGTTGATACTTAGTAAC 956
          |||||||||||||||||||||||
Db    823 TTGTTCGGTTGATACTTAGTAAC 845


RESULT 11
US-09-442-013-9
; Sequence 9, Application US/09442013
; GENERAL INFORMATION:
;  APPLICANT:  Lou, Ying
;  APPLICANT:  Xu, Xiang
;  APPLICANT:  Leo, Cindy
;  APPLICANT:  Huang, Betty
;  APPLICANT:  Shen, Mary
;  TITLE OF INVENTION:  NOVEL IAPS ASSOCIATED CELL CYCLE PROTEINS, COMPOSITIONS
;  TITLE OF INVENTION:  AND METHODS OF USE
;  FILE REFERENCE:  A-68289/DJB/RMS/DAV
;  CURRENT APPLICATION NUMBER: US/09/442,013
;  CURRENT FILING DATE:  1999-11-17
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 958
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-442-013-9

  Query Match             67.6%;  Score 647.4;  DB 18;  Length 958;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-163;
  Matches  651;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    149 TGGAGGCCTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGAT 208
          ||  ||  | | ||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCTGGGATTACAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGAT 360

Qy    209 GCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGA 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGA 420

Qy    269 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGAT 480

Qy    329 CCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCA 388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCA 540

Qy    389 GACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGA 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGA 600

Qy    449 AGCAGATCTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTT 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGCAGATCTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTT 660

Qy    509 AAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATC 720

Qy    569 AGAGGAAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCAT 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGAGGAAGACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCAT 780

Qy    629 CCTGTCCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTA 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCTGTCCGTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTA 840

Qy    689 CTGCCTGTGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCC 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CTGCCTGTGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCC 900

Qy    749 AATTGAGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATG 805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATTGAGTGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATG 957


RESULT 12
US-60-184-797-652
; Sequence 652, Application US/60184797
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                Jones, Anissa L.
;  APPLICANT: Lincoln, Stephen E.          Yu, Jimmy Y.
```

```
;  APPLICANT: Russo, Frank D.                    Greenawalt, Lila B.
;  APPLICANT: Spiro, Peter A.                    Panzer, Scott R.
;  APPLICANT: Banville, Steve C.              Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.              Wright, Rachel J.
;  APPLICANT: Dufour, Gerard E.                  Chen, Wensheng
;  APPLICANT: Cohen, Howard J.                   Liu, Tommy
;  APPLICANT: Rosen, Bruce                    Yap, Pierre E.
;  APPLICANT: Shah, Purvi                        Stockdreher, Theresa K.
;  APPLICANT: Chalup, Michael S.              Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.               Fong, Willy Tuen
;  TITLE OF INVENTION: MOLECULES ASSOCIATED WITH GROWTH AND DEVELOPMENT
;  FILE REFERENCE: PT-0114 P
;  CURRENT APPLICATION NUMBER: US/60/184,797
;  CURRENT FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 1667
;  SOFTWARE: PERL Program
; SEQ ID NO 652
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 121128.14
US-60-184-797-652

  Query Match            67.4%;  Score 645.6;  DB 62;  Length 1275;
  Best Local Similarity  99.4%;  Pred. No. 6.4e-163;
  Matches  648;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     56 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 115

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    116 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 175

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 235

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 295

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 355

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 415

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 475

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    476 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 535

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 595

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    596 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 655

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGT 807
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Db    656 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGT 707
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RESULT 13
US-60-278-258-16936
; Sequence 16936, Application US/60278258
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION:  Polynucleotide Sequence Databases, and Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms Identified Thereby
;  FILE REFERENCE: GX-0010-1 P
;  CURRENT APPLICATION NUMBER: US/60/278,258
;  CURRENT FILING DATE:  2001-03-23
;  NUMBER OF SEQ ID NOS: 17730
;  SOFTWARE: PERL Program
; SEQ ID NO 16936
;   LENGTH: 1275
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 121128.14
US-60-278-258-16936

  Query Match            67.4%;  Score 645.6;  DB 71;  Length 1275;
  Best Local Similarity  99.4%;  Pred. No. 6.4e-163;
  Matches  648;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
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Db     56 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 115

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    116 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 175

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    176 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 235

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    236 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 295

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    296 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 355

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    356 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 415

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    416 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 475

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Db    476 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 535

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    536 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 595

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    596 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 655

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGT 807
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    656 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGT 707
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RESULT 14
PCT-US01-04098A-646
; Sequence 646, Application PC/TUS0104098A
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-029
;  CURRENT APPLICATION NUMBER: PCT/US01/04098A
;  CURRENT FILING DATE:  2001-02-05
;  PRIOR APPLICATION NUMBER: Not Yet Assigned
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 09/728,422
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: 09/693,325
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/663,561
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: 09/654,936
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: 09/620,325
;  PRIOR FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 09/598,075
;  PRIOR FILING DATE: 2000-06-20
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 3960
;  SOFTWARE: Custom
; SEQ ID NO 646
;   LENGTH: 1465
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (251)..(931)
PCT-US01-04098A-646

  Query Match             67.0%;  Score 641.8;  DB 1;  Length 1465;
  Best Local Similarity   98.9%;  Pred. No. 7.1e-162;
  Matches  646;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 340

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 400

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 460

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 520

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 580

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 640

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    641 GGCCTGCGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 700

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Db    701 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 760

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    761 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 820

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 880

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTT 808
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Db    881 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGATT 933


RESULT 15
US-09-620-325-298
; Sequence 298, Application US/09620325
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Tillinghast, John
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 787CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,325
;  CURRENT FILING DATE:  2000-04-27
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 419
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 298
;   LENGTH: 1465
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (251)..(931)
US-09-620-325-298

  Query Match             67.0%;  Score 641.8;  DB 24;  Length 1465;
  Best Local Similarity   98.9%;  Pred. No. 7.1e-162;
  Matches  646;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
          |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 CTGGACAGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 340

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 400

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 460

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
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Db    461 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 520

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 580

Qy    456 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 CTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 640

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    641 GGCCTGCGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 700

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 760

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 820

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    821 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 880

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGGTT 808
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Db    881 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAATGATT 933
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Search completed: February 22, 2003, 22:02:55
Job time : 4166 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	113	11.8	8487	10	US-09-764-877-3454	Sequence 3454, Ap
	2	97	10.1	840	12	US-10-115-899-6	Sequence 6, Appli
	3	97	10.1	1078	12	US-10-115-899-7	Sequence 7, Appli
c	4	75.8	7.9	754	10	US-09-731-872-187	Sequence 187, App
	5	65.2	6.8	813	9	US-09-938-842A-1178	Sequence 1178, Ap
	6	59.8	6.2	352	10	US-09-867-701-2399	Sequence 2399, Ap
	7	52	5.4	993	10	US-09-801-368-257	Sequence 257, App
	8	41.6	4.3	450	10	US-09-867-550-223	Sequence 223, App
	9	41	4.3	846	10	US-09-867-550-1931	Sequence 1931, Ap
c	10	40	4.2	454	10	US-09-864-761-19549	Sequence 19549, A
	11	39	4.1	451	9	US-09-854-133-146	Sequence 146, App
	12	39	4.1	451	10	US-09-738-973-146	Sequence 146, App
	13	37.8	3.9	398	10	US-09-960-352-8059	Sequence 8059, Ap
c	14	37.6	3.9	659158	9	US-09-771-208-20	Sequence 20, Appl
	15	36.8	3.8	368	10	US-09-878-574-1665	Sequence 1665, Ap
	16	36.8	3.8	387	10	US-09-878-574-1404	Sequence 1404, Ap
	17	36.8	3.8	448	10	US-09-960-352-5218	Sequence 5218, Ap
	18	36.8	3.8	643	10	US-09-764-869-577	Sequence 577, App
	19	36.8	3.8	1329	10	US-09-815-242-4023	Sequence 4023, Ap
	20	36.2	3.8	421	10	US-09-960-352-14430	Sequence 14430, A
	21	36	3.8	415	10	US-09-960-352-2580	Sequence 2580, Ap
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c	23	35.8	3.7	3416	8	US-08-987-689A-1	Sequence 1, Appli
c	24	35.4	3.7	475	10	US-09-864-761-6203	Sequence 6203, Ap
c	25	35.4	3.7	511	10	US-09-864-761-22817	Sequence 22817, A
	26	35.4	3.7	1209	10	US-09-815-242-9956	Sequence 9956, Ap
	27	35	3.7	343	10	US-09-960-352-4500	Sequence 4500, Ap
	28	34.4	3.6	420	10	US-09-960-352-9532	Sequence 9532, Ap
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	32	34	3.5	4796	10	US-09-764-847-1627	Sequence 1627, Ap
	33	34	3.5	5835	9	US-09-927-597-1	Sequence 1, Appli
	34	34	3.5	5937	9	US-09-927-597-3	Sequence 3, Appli
	35	34	3.5	13337	10	US-09-764-846-312	Sequence 312, App
	36	34	3.5	13337	10	US-09-764-847-1629	Sequence 1629, Ap
	37	34	3.5	88421	9	US-09-976-059-1	Sequence 1, Appli
	38	33.8	3.5	394	10	US-09-864-761-18958	Sequence 18958, A
	39	33.6	3.5	215	10	US-09-867-701-9278	Sequence 9278, Ap
	40	33	3.4	417	10	US-09-960-352-13113	Sequence 13113, A
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c	42	33	3.4	493	10	US-09-864-761-29936	Sequence 29936, A
c	43	33	3.4	599	10	US-09-864-761-13376	Sequence 13376, A
c	44	33	3.4	2489	10	US-09-764-864-552	Sequence 552, App
	45	33	3.4	2504	10	US-09-764-864-103	Sequence 103, App

ALIGNMENTS

RESULT 1
US-09-764-877-3454
; Sequence 3454, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3454
; LENGTH: 8487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3454

Query Match 11.8%; Score 113; DB 10; Length 8487;
Best Local Similarity 72.6%; Pred. No. 5.9e-23;
Matches 146; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
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Db    6700 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 6759

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db    6760 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 6819

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
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Db    6820 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 6879

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
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Db    6880 AAGACCATGGACAAAGCCCTG 6900
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RESULT 2
US-10-115-899-6

```
; Sequence 6, Application US/10115899
; Patent No. US20020151025A1
; GENERAL INFORMATION:
;  APPLICANT: Ostuka Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
;  FILE REFERENCE: Q60193
;  CURRENT APPLICATION NUMBER: US/10/115,899
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/601,478
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP H10-134679
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: JP H10-73234
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: JP H10-38133
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 840
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human embryonic brain cDNA library
US-10-115-899-6

  Query Match             10.1%;  Score 97;  DB 12;  Length 840;
  Best Local Similarity   68.9%;  Pred. No. 9.5e-19;
  Matches  133;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy     655 TGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATG 714
           | ||  |  |  | || || || ||||| || |||||| | ||| |||| || || ||||
Db     608 TTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATG 667

Qy     715 GGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCG 774
           |||||||||| || |||||||||  | | |||||||||| |||||||||||| | || |
Db     668 GGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTG 727

Qy     775 TGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGA 834
           |    ||||||   ||||| || || |||||||  || |||  |||       || ||
Db     728 TTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATG 787

Qy     835 GGAAGAAGAAGTA 847
           ||| |  | | |
Db     788 AGAAAACAATGGA 800


RESULT 3
US-10-115-899-7
; Sequence 7, Application US/10115899
; Patent No. US20020151025A1
; GENERAL INFORMATION:
;  APPLICANT: Ostuka Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION: Human TSC403 gene and human ING1L gene
;  FILE REFERENCE: Q60193
;  CURRENT APPLICATION NUMBER: US/10/115,899
;  CURRENT FILING DATE:  2002-04-05
;  PRIOR APPLICATION NUMBER: 09/601,478
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: JP H10-134679
;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: JP H10-73234
;  PRIOR FILING DATE: 1998-03-05
;  PRIOR APPLICATION NUMBER: JP H10-38133
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 1078
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human embryonic brain cDNA library
;   NAME/KEY: CDS
;   LOCATION: (92)..(931)
US-10-115-899-7

  Query Match             10.1%;  Score 97;  DB 12;  Length 1078;
  Best Local Similarity   68.9%;  Pred. No. 1.1e-18;
  Matches  133;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy     655 TGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATG 714
           | ||  |  |  | || || || ||||| || |||||| | ||| |||| || || ||||
Db     699 TTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATG 758

Qy     715 GGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCG 774
           |||||||||| || |||||||||  | | |||||||||| |||||||||||| | || |
Db     759 GGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTG 818

Qy     775 TGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGA 834
           |    ||||||   ||||| || || |||||||  || |||  |||       || ||
Db     819 TTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATG 878

Qy     835 GGAAGAAGAAGTA 847
           ||| |  | | |
Db     879 AGAAAACAATGGA 891


RESULT 4
US-09-731-872-187/c
; Sequence 187, Application US/09731872
; Patent No. US20020102604A1
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Bougueleret, Lydie
;  APPLICANT:  Jobert, Severin
;  TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS
;  FILE REFERENCE: 78.US3.REG
;  CURRENT APPLICATION NUMBER: US/09/731,872
;  CURRENT FILING DATE:  2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/169,629
;  PRIOR FILING DATE: 1999-12-08
;  PRIOR APPLICATION NUMBER: US 60/187,470
;  PRIOR FILING DATE: 2000-03-06
;  NUMBER OF SEQ ID NOS: 482
;  SOFTWARE: Patent.pm
; SEQ ID NO 187
;   LENGTH: 754
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 181..462
US-09-731-872-187

  Query Match             7.9%;  Score 75.8;  DB 10;  Length 754;
  Best Local Similarity   75.7%;  Pred. No. 1.6e-12;
  Matches  137;  Conservative    0;  Mismatches   32;  Indels   12;  Gaps    3;

Qy     776 GGACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAG 835
           |||||||||| | || ||| ||| |||||| ||||||||||||||||||||||||  ||
Db     294 GGACCTTACCATG-AATCCAGAGGGAAATGGGTCTGTCCACGGTGTGTCCAGGAAAGCAG 236

Qy     836 GAAGAAGAAGTAGGAGGAGCTGTGTGCCCGGATCCGAGGAGCAAGTTAATCTGTCCCTTC 895
           |||||||  | |||   |||||| |||| |  ||  ||         | ||| || |||
Db     235 GAAGAAG--GAAGGGAAAGCTGTATGCCAGATTCAAAG---------AGTCTATCTCTTT 187

Qy     896 ATTCGTGTCGCAATATTTCCCTTCCTTTTAAAACTACCTTGTTCGGTTGATACTTAGTAA 955
           |||| ||| |||| |||| | ||| ||||||||||||||||||  ||||||  || |||
Db     186 ATTCATGTTGCAAGATTTTCTTTCATTTTAAAACTACCTTGTTCAATTGATATGTAATAA 127

Qy     956 C 956
           |
Db     126 C 126
```

```
RESULT 5
US-09-938-842A-1178
; Sequence 1178, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
;  APPLICANT: Harper, Jeff
;  APPLICANT:  Kreps, Joel
;  APPLICANT:  Wang, Xun
;  APPLICANT:  Zhu, Tong
;  TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
;  TITLE OF INVENTION:  SAME, AND METHODS OF USE
;  FILE REFERENCE: SCRIP1300-3
;  CURRENT APPLICATION NUMBER: US/09/938,842A
;  CURRENT FILING DATE:  2001-08-24
;  PRIOR APPLICATION NUMBER: US 60/227,866
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: US 60/264,647
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/300,111
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1178
;   LENGTH: 813
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-1178

  Query Match             6.8%;  Score 65.2;  DB 9;  Length 813;
  Best Local Similarity   67.7%;  Pred. No. 2.3e-09;
  Matches  107;  Conservative    0;  Mismatches   48;  Indels    3;  Gaps    1;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||   |||  | || ||||||||||| || |||||  | ||||| ||||| |||| |||
Db     550 GAGCAGCCAATCGATCCAAACGAACCAACTTACTGTGTCTGCCATCAGGTGTCCTTTGGA 609

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTC---CAATTGAGTGGTTTCACTTTGCCTGC 773
           || ||||||| ||||||||||    | || |    |  ||| ||||||||||| | | |||
Db     610 GACATGATTGCCTGTGACAATGAGAATTGCCAAGGAGGTGAATGGTTTCACTATACATGC 669

Qy     774 GTGGACCTTACCACGAAACCCAAAGGAAAATGGTTCTG 811
           || | ||| ||  |  |  ||| |  ||| ||   ||
Db     670 GTTGGCCTCACACCTGAGACCAGATTCAAAGGGAAATG 707


RESULT 6
US-09-867-701-2399
; Sequence 2399, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Aglate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2399
;   LENGTH: 352
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(352)
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2399

  Query Match             6.2%;  Score 59.8;  DB 10;  Length 352;
  Best Local Similarity   50.9%;  Pred. No. 5.8e-08;
  Matches  139;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy     156 CTGATAGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAG 215
           |||  |   || ||| | |||||    || || | |      |||  |   ||||| |||
Db      80 CTGGAAATGATTGAGCAGCTTCCTATGGATCTGCGGGACCNTTTCACGGAAATGCGCGAG 139

Qy     216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
           |||||| |  |  | |  || |    |  | | ||       |     || | | |
Db     140 ATGGACCTGCAGGTGCAGAATNAATTGGATCAACTAGAACAAAGAGTCAGTGAATTCTTT 199

Qy     276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
             |  | ||||        || ||   | | |  ||||   ||      ||| | ||
Db     200 ATGAATGCAAAGAAAAATAAACCTGAGTGGAGGGAAGAGCAAATGGCATCCATCAAAAAA 259

Qy     336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
           | ||||   ||      |||| |    || || || || ||| |||| |  ||||  ||
Db     260 GACTACTATAAAGCTTTGGAAGATGCAGATGAGAAGGTTCAGTTGGCAAACCAGATATAT 319

Qy     396 GAGATGGTGGATAAACACATTCGAAGGCTTGAT 428
           ||  |||| |||  |||| |  ||| ||| |||
Db     320 GACTTGGTAGATCGACACTTGAGAAAGCTGGAT 352


RESULT 7
US-09-801-368-257
; Sequence 257, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
;  APPLICANT: Busby, Robert
;  APPLICANT:  Cali, Brian
;  APPLICANT:  Hecht, Peter
;  APPLICANT:  Holtzman, Doug
;  APPLICANT:  Madden, Kevin
;  APPLICANT:  Maxon, Mary
;  APPLICANT:  Milne, Todd
;  APPLICANT:  No. US20020128250A1man, Thea
;  APPLICANT:  Royer, John
;  APPLICANT:  Salama, Sofie
;  APPLICANT:  Sherman, Amir
;  APPLICANT:  Silva, Jeff
;  APPLICANT:  Summers, Eric
;  TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
;  FILE REFERENCE: 109272.147
;  CURRENT APPLICATION NUMBER: US/09/801,368
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 09/487,558
;  PRIOR FILING DATE: 2000-01-19
;  PRIOR APPLICATION NUMBER: US 60/160,587
;  PRIOR FILING DATE: 1999-10-20
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 257
;   LENGTH: 993
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-801-368-257

  Query Match             5.4%;  Score 52;  DB 10;  Length 993;
  Best Local Similarity   59.5%;  Pred. No. 2e-05;
  Matches   88;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy     664 CCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGGGAGATGA 723
           ||   |||     ||||||    ||||||   ||  |||| ||  | || ||||| |||
Db     821 CCAACGACTACGGCGAACCGCTCTACTGCTACTGTAACCAAGTGGCATACGGGGAAATGG 880

Qy     724 TTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTGGACCTTA 783
           | || |||||     ||||||||    | || ||||| || ||  | ||  | |  ||
Db     881 TGGGGTGTGATGGCGCAGACTGTGAGCTAGAATGGTTCCATTTGCCATGTATTGGACTCG 940

Qy     784 CCACGAAACCCAAAGGAAAATGGTTCTG 811
             ||   ||| || || || ||||  ||
Db     941 AAACTCTACCTAAGGGCAAGTGGTATTG 968


RESULT 8
```

```
US-09-867-550-223
; Sequence 223, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin D.
;  APPLICANT:  Mehraban, Fuad,
;  APPLICANT:  Conley, Pamela
;  APPLICANT:  Law, Debbie
;  APPLICANT:  Topper, James
;  TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 21402-013 (Cura-313)
;  CURRENT APPLICATION NUMBER: US/09/867,550
;  CURRENT FILING DATE:  2001-09-20
;  PRIOR APPLICATION NUMBER: USSN 60/208,427
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 2125
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 223
;   LENGTH: 450
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(31)
;   OTHER INFORMATION: wherein any n is one of a or t or g or c
US-09-867-550-223

  Query Match             4.3%;  Score 41.6;  DB 10;  Length 450;
  Best Local Similarity   50.2%;  Pred. No. 0.016;
  Matches  101;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy    201 CAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTG 260
          | | || |     |  ||||   |   |  |  |  | | | |  ||||    |||||
Db     25 CGGGTGNTCACCCACATGGAGTCGGAAATCGGCGTCATGCAGGTGGAGAAGCGCATCCGC 84

Qy    261 GCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTG 320
            | | |       | || |||||||| |     | || | | |   ||||   ||
Db     85 AACCGCGTGAAGCGGCAGATGGAGAAGACGCAGCGCGAATACTACCTCAACGAGCAGATG 144

Qy    321 CAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTG 380
           ||  |||||||||| |    | || || || |||||  | | ||||| |  |   || |
Db    145 AAGGCGATCCAGAAGGAGCTCGGCGAGGGCGAGGAAGGCCGCGACGAGACCGCCGAGATC 204

Qy    381 GCCATGCAGACCTACGAGATG 401
          |    | ||| | |  ||| |
Db    205 GAGGAGAAGATCAAGAAGACG 225


RESULT 9
US-09-867-550-1931
; Sequence 1931, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
;  APPLICANT: Leach, Martin D.
;  APPLICANT:  Mehraban, Fuad,
;  APPLICANT:  Conley, Pamela
;  APPLICANT:  Law, Debbie
;  APPLICANT:  Topper, James
;  TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
;  TITLE OF INVENTION:  Thereby
;  FILE REFERENCE: 21402-013 (Cura-313)
;  CURRENT APPLICATION NUMBER: US/09/867,550
;  CURRENT FILING DATE:  2001-09-20
;  PRIOR APPLICATION NUMBER: USSN 60/208,427
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 2125
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1931
;   LENGTH: 846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-867-550-1931

  Query Match             4.3%;  Score 41;  DB 10;  Length 846;
  Best Local Similarity   50.8%;  Pred. No. 0.033;
  Matches   98;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy    468 ATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGAGGGTTAAAAAAAGGCCGGGGTCAG 527
          | |  ||  |   ||  || ||| ||  || ||| ||| ||||| |||||| |
Db    436 AGGTTGGTGATAAATCATGGAAGGTCTTGAAGGCCAGGCTTAAATAAAGGCAGCATGTGA 495

Qy    528 AAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAAGACACACCAAAG 587
          |  ||      || || |  || |||| |  |  ||   |  ||| |   |||  ||
Db    496 GAGAAAGTTCTTGGCTCACTAGGGCGAGACCTGGAGAAGCCGAAGGTAAGAACATGAAGT 555

Qy    588 AAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCCGTGCACCCCTCT 647
            |   |||   |||   |||      ||| | |  ||| | | |  | |  | |||||
Db    556 GCAGTACAGCCACAAGACAGGTAGTGACTCATTCATCCCAGCTTCTTTGGGGCCACCTCT 615

Qy    648 GATGTGCTGGACA 660
          || |    ||||
Db    616 TATCTATGAGACA 628


RESULT 10
US-09-864-761-19549/c
; Sequence 19549, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
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;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19549
;   LENGTH: 454
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC006371.2
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
;   OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.4
;   OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL =   3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
;   OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
;   OTHER INFORMATION: EST_HUMAN HIT: AW900281.1, EVALUE 7.30e-02
;   OTHER INFORMATION: NT HIT: Y12488.1, EVALUE 4.50e+00
;   OTHER INFORMATION: SWISSPROT HIT: O68827, EVALUE 7.80e+00
US-09-864-761-19549

  Query Match             4.2%;  Score 40;  DB 10;  Length 454;
  Best Local Similarity   48.7%;  Pred. No. 0.047;
  Matches  109;  Conservative    0;  Mismatches  115;  Indels    0;  Gaps    0;

Qy    384 ATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGC 443
          | | |||   | |||| || |   ||  | |   | |     || |  ||   |  |
Db    451 AGGAAGAAGGAGGAGAAGGAGAGGAAGAAGAAGAGGAAAAAGGAGGAGGAGGAGAGGAAG 392

Qy    444 TTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGTGATTTTGAAAGCTCCGGAGGGCGA 503
             || |  ||   |||||| |||| ||| |     ||    ||| |    ||||   ||
Db    391 AAGGAGGAGGAGGAGAAGGAGAAGAAGGAAGAGGAAGAAGAAGAAGGAGAAGGAGAAAGA 332

Qy    504 GGGTTAAAAAAAGGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGG 563
          ||   |  || |||  | ||      || || | |||       ||    |||  |  |
Db    331 GGAGGAGGAAGAGGAGGAGGAAGAGGAGGAAGAGGAGAAGAGGAGGAGGAAGGAGGAGGA 272

Qy    564 ACATCAGAGGAAGACACACCAAAGAAAAAGAAGCACAAAGGAGG 607
          | |     |      | |  |||||| |||||| | ||||||||
Db    271 AGAAGGAGGAGGAGAAGAAGAAAGAAGAAGAAGAAGAAAGGAGG 228


RESULT 11
US-09-854-133-146
; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
;  APPLICANT: Lodes, Michael J.
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  THE THERAPY AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.475C10
;  CURRENT APPLICATION NUMBER: US/09/854,133
;  CURRENT FILING DATE:  2001-05-11
;  NUMBER OF SEQ ID NOS: 735
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 146
;   LENGTH: 451
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-854-133-146

  Query Match             4.1%;  Score 39;  DB 9;  Length 451;
  Best Local Similarity   48.5%;  Pred. No. 0.092;
  Matches  146;  Conservative    0;  Mismatches  145;  Indels   10;  Gaps    1;

Qy    161 AGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGA 220
          ||  ||||||  ||| || | |||  | ||||| ||  ||  ||||||||| ||| | ||
Db     13 AGCCATCGAGTCCCTGCCTTTCGACTTGCAGAGAAATGTCTCGCTGATGCGGGAGATCGA 72

Qy    221 CCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCAC 280
          |  ||      |||| |         ||| | |||          |      | ||    |
Db     73 CGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGA 132

Qy    281 GGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTA 340
          |    |   | |         | |    || |  |  |||||       | || |  |
Db    133 GACAGACGGGGCGCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGCAC 192

Qy    341 CAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGAT 400
          ||| |  ||           | ||||| ||  | ||| | |  |  ||||     ||| |
Db    193 CAGGAGCTG----------GGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCT 242

Qy    401 GGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAA 460
          |||||| || | ||  ||   | | ||     || ||| ||  || || ||  | | | |
Db    243 GGTGGAGAACCGCACGCGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGA 302

Qy    461 G 461
          |
Db    303 G 303


RESULT 12
US-09-738-973-146
; Sequence 146, Application US/09738973
; Patent No. US20020110563A1
; GENERAL INFORMATION:
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Fling, Steven P.
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Algate, Paul A.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Indirias, Carol Yoseph
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Elliot, Mark
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Kalos, Michael D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  THE THERAPY AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.475C9
;  CURRENT APPLICATION NUMBER: US/09/738,973
;  CURRENT FILING DATE:  2000-12-14
;  NUMBER OF SEQ ID NOS:  587
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 146
;   LENGTH: 451
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-738-973-146

  Query Match             4.1%;  Score 39;  DB 10;  Length 451;
  Best Local Similarity   48.5%;  Pred. No. 0.092;
  Matches  146;  Conservative    0;  Mismatches  145;  Indels   10;  Gaps    1;

Qy    161 AGGTATCGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGA 220
          ||  ||||||  ||| || | |||  | ||||| ||  ||  ||||||||| ||| | ||
Db     13 AGCCATCGAGTCCCTGCCTTTCGACTTGCAGAGAAATGTCTCGCTGATGCGGGAGATCGA 72

Qy    221 CCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCAC 280
          |  ||      |||| |         ||| | |||          |      | ||    |
Db     73 CGCGAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGA 132

Qy    281 GGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTA 340
          |    |   | |         | |    || |  |  |||||       | || |  |
Db    133 GACAGACGGGGCGCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGCAC 192

Qy    341 CAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGAT 400
          ||| |  ||           | ||||| ||  | ||| | |  |  ||||     ||| |
Db    193 CAGGAGCTG----------GGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCT 242

Qy    401 GGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAA 460
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          |||||| || | ||  ||   | | ||     || ||| ||  || || ||  | | | |
Db    243 GGTGGAGAACCGCACGCGGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGA 302

Qy    461 G 461
          |
Db    303 G 303


RESULT 13
US-09-960-352-8059
; Sequence 8059, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8059
;   LENGTH: 398
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 35-BOVMS1-019-Q1-E1-A4
US-09-960-352-8059

  Query Match             3.9%;  Score 37.8;  DB 10;  Length 398;
  Best Local Similarity   46.4%;  Pred. No. 0.19;
  Matches  123;  Conservative    0;  Mismatches  142;  Indels    0;  Gaps    0;

Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
          | |||     | |  | |||  |||||||  |||  | ||||   | |||||     ||
Db     48 CAGGAAGCTCGCAACGCAGAAGAGAAAGCCAAGAAGGCCATCACTGATGCAGCCATGATG 107

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
          |   || |  || | |   |  |||    |||   | |    || || ||   |||||
Db    108 GCTGAGGAGCTGAAGAAGGAGCAGGACACCAGCGCCCACCTGGAGCGGATGAAGAAGAAC 167

Qy    336 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 395
          |    | |  |||||        ||      |   ||   ||    || | ||
Db    168 ATGGAGCAGACGGTGAAGGACCTGCAGAACCGTCTGGATGAGGCTGAGCAGCTGGCCCTG 227

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
          ||   | | | || || || |  |  || || ||  |  ||       | |||| |||
Db    228 AAGGGCGGGAAGAAGCAGATCCAGAAACTGGAGGCCAAGGTGCGTGAGCTGGAAGGAGAG 287

Qy    456 CTGAAGGACAAGATGGAGGGCAGTG 480
          |  ||    ||  | || ||| ||
Db    288 GTATAGAGTGAGCAGAAGCGCAATG 312


RESULT 14
US-09-771-208-20/c
; Sequence 20, Application US/09771208
; Patent No. US20020155564A1
; GENERAL INFORMATION:
;  APPLICANT: MEDRANO, JUAN
;  APPLICANT:  BRADFORD, ERIC
;  APPLICANT:  HORVAT, SIMON
;  TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
;  FILE REFERENCE: 407T-923710US
;  CURRENT APPLICATION NUMBER: US/09/771,208
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: US 08/999,477
;  PRIOR FILING DATE: 1997-12-29
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 659158
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (123459)..(123478)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (602466)..(602485)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (546998)..(547017)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (494715)..(494814)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (390986)..(391005)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (346860)..(346823)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (317174)..(317193)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (280353)..(280373)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (271829)..(271848)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (183872)..(183891)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (170625)..(170645)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   LOCATION: (132680)..(132700)
;   OTHER INFORMATION: n is unidentified a, c, g, or t
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: n is a, c, g, or t
US-09-771-208-20

  Query Match             3.9%;  Score 37.6;  DB 9;  Length 659158;
  Best Local Similarity   45.1%;  Pred. No. 10;
  Matches  139;  Conservative    0;  Mismatches  169;  Indels    0;  Gaps    0;

Qy    167 CGAGAACCTTCCCTGCGAACTTCAGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAG 226
          || ||||||||| |  |   ||     |  |  |  |||  ||  | | | |  ||| |
Db 251205 CGTGAACCTTCTCCCCATTCTAACTGGTCAAATAAGGCTAGAGCCTGTGATTGGGCAGTG 251146

Qy    227 GACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAA 286
          || || | |   || |   ||| |          |   |  ||| |         | | |
Db 251145 GAAGGCAAAGGTGAGATGGGAGGTCTTAGAGAGGAAGGAGGAGGAAGAGGAGGAAGAGGA 251086

Qy    287 GACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAA 346
          |  || |      || |||   | ||||   | | || ||    || | |   |     |
Db 251085 GGAGCAGGAGGAGGAGCAGGAGGAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAAGAAGA 251026

Qy    347 GTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGA 406
          |    |||| |    || ||  | | | ||| ||    | ||    | |||  || |||
Db 251025 GGAGGAGGAGGAAGAAGAGGAGGAGGAGGAGCAGGAGGAGGAGGAGCAGGAGGAGGAGGA 250966

Qy    407 TAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGATCTGAAGGACAA 466
            | ||          |   || | |||   || |      ||||  ||   | ||||  |
Db 250965 GGAGCAGGAGGAGGAGGAGGAGGAAGAGGAGGAGAAGGAGGAAGAGGAGGAGGAGGAGGA 250906

Qy    467 GATGGAGG 474
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Db 250905 GGAGGAGG 250898


RESULT 15
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US-09-878-574-1665
; Sequence 1665, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1665
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-034-Q1-B1-H7
US-09-878-574-1665

Query Match 3.8%; Score 36.8; DB 10; Length 368;
Best Local Similarity 47.1%; Pred. No. 0.37;
Matches 113; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy    190 AGAGGAACTTCCAGCTGATGCGAGAGCTGGACCAGAGGACGGAAGATAAGAAAGCAGAGA 249
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Db     95 AGAAGAAGTTCGAGCCGGCGGCGCCGCCGGCCCGCGTGGGCCGTAAGCAGCGTAAGCAGA 154

Qy    250 TTGACATCCTGGCTGCAGAGTACATCTCCACGGTGAAGACGCTGTCTCCAGACCAGCGCG 309
            | |     ||| || | |    |  | |||||||| | |||||||      | |||
Db    155 AGGGCCCGGAGGCGGCGGCGCGGCTGCCGACGGTGACGCCGCTGTCGAAGTGCAAGCTAA 214

Qy    310 TGGAGCGCCTGCAGAAGATCCAGAACGCCTACAGCAAGTGCAAGGAATACAGTGACGACA 369
           |  ||    || | ||  |   || | ||||  |  |    ||||  |    |  |  |
Db    215 GGCTGCTGAAGCTGGAGCGCATAAAGGACTACCTCTTGATGGAGGAGGAGTTCGTGGCGA 274

Qy    370 AAGTGCAGCTGGCCATGCAGACCTACGAGATGGTGGATAAACACATTCGAAGGCTTGATG 429
          |   | ||  |   | || |    | |||| ||  ||  || |||     | | | ||||
Db    275 ACCAGGAGAGGCTGAAGCCGCAGGAGGAGAAGGCCGAGGAAGACAGATCCAAGGTCGATG 334
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Search completed: February 22, 2003, 22:19:01
Job time : 642 secs

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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-7400
;      TELEFAX:  415-854-8275
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  16..900
US-09-258-372-9

  Query Match             11.8%;  Score 113;  DB 4;  Length 2061;
  Best Local Similarity   72.6%;  Pred. No. 2.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||||| |||||| |||||||||||||||||
Db     664 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 723

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     724 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 783

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 843

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     844 AAGACCATGGACAAAGCCCTG 864


RESULT 15
US-09-006-783A-2
; Sequence 2, Application US/09006783A
; Patent No. 6297366
;  GENERAL INFORMATION:
;    APPLICANT:  Gudkov, Andrey V
;    APPLICANT:  Garkavstev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  p33/ING1 as a Mediator of p53 Signaling
;    TITLE OF INVENTION:  Pathway
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,783A
;      FILING DATE:  15-JAN-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6297366nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  97,837
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  16..897
US-09-006-783A-2

  Query Match             11.8%;  Score 113;  DB 4;  Length 2061;
  Best Local Similarity   72.6%;  Pred. No. 2.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||||| |||||| |||||||||||||||||
Db     664 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 723

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     724 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 783

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 843

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     844 AAGACCATGGACAAAGCCCTG 864


Search completed: February 22, 2003, 20:53:20
Job time : 73 secs
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/569721
;      FILING DATE:  08-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-7400
;      TELEFAX:  415-854-8275
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  16..900
US-08-751-230-9

  Query Match             11.8%;  Score 113;  DB 3;  Length 2061;
  Best Local Similarity   72.6%;  Pred. No. 2.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||| |||||| ||||||||||||||||
Db     664 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 723

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     724 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 783

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||       ||| ||   |
Db     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 843

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     844 AAGACCATGGACAAAGCCCTG 864


RESULT 13
US-09-499-082-9
; Sequence 9, Application US/09499082
; Patent No. 6143522
;  GENERAL INFORMATION:
;    APPLICANT:  Helbing, Caren C.
;    APPLICANT:  Riabowol, Karl
;    APPLICANT:  Johnston, Randall N.
;    APPLICANT:  Garkavtsev, Igor
;    TITLE OF INVENTION:  METHODS OF MODULATING APOPTOSIS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/499,082
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/828,158
;      FILING DATE:  27-MAR-1997
;      APPLICATION NUMBER:  US 08/751230
;      FILING DATE:  15-NOV-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/569721
;      FILING DATE:  08-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-854-7400
;      TELEFAX:  650-854-8275
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  16..900
US-09-499-082-9

  Query Match             11.8%;  Score 113;  DB 3;  Length 2061;
  Best Local Similarity   72.6%;  Pred. No. 2.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||| |||||| ||||||||||||||||
Db     664 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 723

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     724 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 783

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||       ||| ||   |
Db     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 843

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     844 AAGACCATGGACAAAGCCCTG 864


RESULT 14
US-09-258-372-9
; Sequence 9, Application US/09258372
; Patent No. 6238918
;  GENERAL INFORMATION:
;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/258,372
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/751,230
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/258,372
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/751,230
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-7400
;      TELEFAX:  415-854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1902 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..741
US-09-258-372-1

  Query Match             11.8%;  Score 113;  DB 4;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||||| |||||| |||||||||||||||||
Db     505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||     ||| ||   |
Db     625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     685 AAGACCATGGACAAAGCCCTG 705


RESULT 11
US-09-258-371-9
; Sequence 9, Application US/09258371
; Patent No. 5986078
;  GENERAL INFORMATION:
;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/258,371
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/751,230
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-7400
;      TELEFAX:  415-854-8275
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2061 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  16..900
US-09-258-371-9

  Query Match             11.8%;  Score 113;  DB 2;  Length 2061;
  Best Local Similarity   72.6%;  Pred. No. 2.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||||| |||||| |||||||||||||||||
Db     664 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 723

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     724 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 783

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||     ||| ||   |
Db     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 843

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     844 AAGACCATGGACAAAGCCCTG 864


RESULT 12
US-08-751-230-9
; Sequence 9, Application US/08751230
; Patent No. 6117633
;  GENERAL INFORMATION:
;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,230
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  514
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;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,230
;       FILING DATE:  15-NOV-1996
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/569721
;       FILING DATE:  08-DEC-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mooi, Leslie A.
;       REGISTRATION NUMBER:  37,047
;       REFERENCE/DOCKET NUMBER:  028722-144
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-854-7400
;       TELEFAX:  415-854-8275
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1902 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  109..741
US-08-751-230-1

  Query Match           11.8%;  Score 113;  DB 3;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| ||||||||||||||||| |||||| ||||||||||||||||
Db     505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 684

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     685 AAGACCATGGACAAAGCCCTG 705


RESULT 9
US-09-499-082-1
; Sequence 1, Application US/09499082
; Patent No. 6143522
;  GENERAL INFORMATION:
;    APPLICANT:  Helbing, Caren C.
;    APPLICANT:  Riabowol, Karl
;    APPLICANT:  Johnston, Randall N.
;    APPLICANT:  Garkavtsev, Igor
;    TITLE OF INVENTION:  METHODS OF MODULATING APOPTOSIS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/499,082
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/828,158
;      FILING DATE:  27-MAR-1997
;      APPLICATION NUMBER:  US 08/751230
;      FILING DATE:  15-NOV-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/569721
;      FILING DATE:  08-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-148
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-854-7400
;      TELEFAX:  650-854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1902 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..741
US-09-499-082-1

  Query Match           11.8%;  Score 113;  DB 3;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| ||||||||||||||||| |||||| ||||||||||||||||
Db     505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     685 AAGACCATGGACAAAGCCCTG 705


RESULT 10
US-09-258-372-1
; Sequence 1, Application US/09258372
; Patent No. 6238918
;  GENERAL INFORMATION:
;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
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;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/258,371
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/751,230
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-7400
;      TELEFAX:  415-854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1902 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..741
US-09-258-371-1

  Query Match             11.8%;  Score 113;  DB 2;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||| |||||| ||||||||||||||||
Db     505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     685 AAGACCATGGACAAAGCCCTG 705


RESULT 7
US-08-569-721A-1
; Sequence 1, Application US/08569721A
; Patent No. 6037121
;  GENERAL INFORMATION:
;    APPLICANT:  GARKAVTSEV, Igor
;    APPLICANT:  RIABOWOL, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING A TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/569,721A
;      FILING DATE:  08-DEC-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-128
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 854-7400
;      TELEFAX:  (650) 854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1902 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..738
US-08-569-721A-1

  Query Match             11.8%;  Score 113;  DB 3;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy     657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
           ||| | ||| | ||||| |||||||||||||||| |||||| ||||||||||||||||
Db     505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy     717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
           |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db     565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy     777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
           |  || |     |||||||| || || |||| ||||||   |||      ||| ||   |
Db     625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG 684

Qy     837 AAGAAGAAGTAGGAGGAGCTG 857
           ||||  | | |  | |  |||
Db     685 AAGACCATGGACAAAGCCCTG 705


RESULT 8
US-08-751-230-1
; Sequence 1, Application US/08751230
; Patent No. 6117633
;  GENERAL INFORMATION:
;    APPLICANT:  Garkavtsev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING THE TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE ING1
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  699 Prince Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
```

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Qy    837 AAGAAGAAGTAGGAGGAGCTG 857
          ||||  | | |  | |  |||
Db    577 AAGACCATGGACAAAGCCCTG 597


RESULT 4
US-09-006-783A-4
; Sequence 4, Application US/09006783A
; Patent No. 6297366
;  GENERAL INFORMATION:
;    APPLICANT:  Gudkov, Andrey V
;    APPLICANT:  Garkavstev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  p33/ING1 as a Mediator of p53 Signaling
;    TITLE OF INVENTION:  Pathway
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,783A
;      FILING DATE:  15-JAN-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6297366nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  97,837
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  873 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  7..813
US-09-006-783A-4

  Query Match             11.8%;  Score 113;  DB 4;  Length 873;
  Best Local Similarity   72.6%;  Pred. No. 1.3e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy    657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
          ||| | ||| | ||||| ||||||||||||||||||| |||||| ||||||||||||||||||
Db    610 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 669

Qy    717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
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Db    670 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 729

Qy    777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
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Db    730 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 789

Qy    837 AAGAAGAAGTAGGAGGAGCTG 857
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Db    790 AAGACCATGGACAAAGCCCTG 810


RESULT 5
US-09-258-257-1
; Sequence 1, Application US/09258257
; Patent No. 5965398
;  GENERAL INFORMATION:
;    APPLICANT:  GARKAVTSEV, Igor
;    APPLICANT:  RIABOWOL, Karl
;    TITLE OF INVENTION:  DNA SEQUENCE ENCODING A TUMOR
;    TITLE OF INVENTION:  SUPPRESSOR GENE
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/258,257
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/569,721
;      FILING DATE:  08-DEC-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mooi, Leslie A.
;      REGISTRATION NUMBER:  37,047
;      REFERENCE/DOCKET NUMBER:  028722-128
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 854-7400
;      TELEFAX:  (650) 854-8275
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1902 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  109..738
US-09-258-257-1

  Query Match             11.8%;  Score 113;  DB 2;  Length 1902;
  Best Local Similarity   72.6%;  Pred. No. 2e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy    657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
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Db    505 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 564

Qy    717 GAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTTCACTTTGCCTGCGTG 776
          |||||||| ||||| |||||    || || || || |||||||| |||||  | ||||||
Db    565 GAGATGATCGGCTGCGACAACGACGAGTGCCCCATCGAGTGGTTCCACTTCTCGTGCGTG 624

Qy    777 GACCTTACCACGAAACCCAAAGGAAAATGGTTCTGTCCACGGTGTGTCCAGGAAAAGAGG 836
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Db    625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGGAGAACGAG 684

Qy    837 AAGAAGAAGTAGGAGGAGCTG 857
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Db    685 AAGACCATGGACAAAGCCCTG 705


RESULT 6
US-09-258-371-1
; Sequence 1, Application US/09258371
; Patent No. 5986078
;  GENERAL INFORMATION:
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Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Db    451 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 510

Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    511 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 570

Qy    696 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 755
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Db    571 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 630

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAA 803
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Db    631 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAA 678


RESULT 2
US-09-195-286-2
; Sequence 2, Application US/09195286
; Patent No. 6066474
; GENERAL INFORMATION:
;  APPLICANT: Marcu, Kenneth B.
;  TITLE OF INVENTION: Y2H56 A STRONG IKK BINDING PROTEIN
;  FILE REFERENCE: Docket No. 6066474 178-258
;  CURRENT APPLICATION NUMBER: US/09/195,286
;  CURRENT FILING DATE: 1998-11-18
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 699
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-195-286-2

  Query Match            66.5%;  Score 636.8;  DB 3;  Length 699;
  Best Local Similarity  98.9%;  Pred. No. 1.5e-183;
  Matches  641;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Db    112 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 171

Qy    276 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 335
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Db    172 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 231

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Db    292 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 351

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Db    352 CTGAAGGACAAGATGGAGGGCAGTGATTTTCAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 411

Qy    516 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 575
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Db    412 GGCCGGGGTCAGAAAGAAAAAAGAGGGTCCCGGGGCCGAGGCAGGAGGACATCAGAGGAA 471

Qy    576 GACACACCAAAGAAAAAGAAGCACAAAGGAGGGTCTGAGTTCACTGACACCATCCTGTCC 635
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Qy    636 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 695
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Db    532 GTGCACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTG 591

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Db    592 TGCCACCAGGTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAG 651

Qy    756 TGGTTTCACTTTGCCTGCGTGGACCTTACCACGAAACCCAAAGGAAAA 803
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RESULT 3
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; Sequence 6, Application US/09006783A
; Patent No. 6297366
;  GENERAL INFORMATION:
;    APPLICANT:  Gudkov, Andrey V
;    APPLICANT:  Garkavstev, Igor
;    APPLICANT:  Riabowol, Karl
;    TITLE OF INVENTION:  p33/ING1 as a Mediator of p53 Signaling
;    TITLE OF INVENTION:  Pathway
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDonnell Boehnen Hulbert & Berghoff
;      STREET:  300 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/006,783A
;      FILING DATE:  15-JAN-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 6297366nan, Kevin E
;      REGISTRATION NUMBER:  35,303
;      REFERENCE/DOCKET NUMBER:  97,837
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-913-0001
;      TELEFAX:  312-913-0002
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..630
US-09-006-783A-6

  Query Match            11.8%;  Score 113;  DB 4;  Length 633;
  Best Local Similarity  72.6%;  Pred. No. 1.1e-24;
  Matches  146;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy    657 GACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAGGTCTCCTATGGG 716
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Db    397 GACCTCCCCATCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG 456

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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

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Title: US-09-442-013-7
Perfect score: 958
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	636.8	66.5	699	3	US-09-195-286-2	Sequence 2, Appli
	3	113	11.8	633	4	US-09-006-783A-6	Sequence 6, Appli
	4	113	11.8	873	4	US-09-006-783A-4	Sequence 4, Appli
	5	113	11.8	1902	2	US-09-258-257-1	Sequence 1, Appli
	6	113	11.8	1902	2	US-09-258-371-1	Sequence 1, Appli
	7	113	11.8	1902	3	US-08-569-721A-1	Sequence 1, Appli
	8	113	11.8	1902	3	US-08-751-230-1	Sequence 1, Appli
	9	113	11.8	1902	3	US-09-499-082-1	Sequence 1, Appli
	10	113	11.8	1902	4	US-09-258-372-1	Sequence 1, Appli
	11	113	11.8	2061	2	US-09-258-371-9	Sequence 9, Appli
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	16	113	11.8	2061	4	US-09-159-871-1	Sequence 1, Appli
	17	97	10.1	840	4	US-09-601-478-6	Sequence 6, Appli
	18	97	10.1	1078	4	US-09-601-478-7	Sequence 7, Appli
	19	97	10.1	1154	4	US-09-484-970B-81	Sequence 81, Appl
c	20	75.8	7.9	7218	1	US-08-232-463-14	Sequence 14, Appl
	21	46.8	4.9	289	4	US-09-007-005-17	Sequence 17, Appl
	22	46.8	4.9	289	4	US-09-244-796-17	Sequence 17, Appl
	23	41.4	4.3	2338	1	US-08-425-069-1	Sequence 1, Appli
	24	41.4	4.3	2338	2	US-08-317-844B-1	Sequence 1, Appli
	25	40.2	4.2	277	4	US-09-007-005-3	Sequence 3, Appli
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	29	39	4.1	451	4	US-09-370-838-146	Sequence 146, App
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	34	37.4	3.9	3588	1	US-08-459-214-32	Sequence 32, Appl
c	35	36.2	3.8	51259	3	US-08-781-891-209	Sequence 209, App
c	36	35.8	3.7	3416	2	US-08-357-642A-2	Sequence 2, Appli
c	37	35.8	3.7	3416	2	US-08-460-626-2	Sequence 2, Appli
c	38	35	3.7	1926	4	US-09-249-585A-4	Sequence 4, Appli
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	40	35	3.7	2576	1	US-08-471-033-35	Sequence 35, Appl
	41	35	3.7	2576	2	US-08-471-044-35	Sequence 35, Appl
	42	35	3.7	2576	2	US-08-463-483A-35	Sequence 35, Appl
	43	35	3.7	2576	2	US-08-471-046A-35	Sequence 35, Appl
	44	35	3.7	2576	2	US-08-470-566B-35	Sequence 35, Appl
	45	35	3.7	2576	2	US-08-469-334-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-195-286-3
; Sequence 3, Application US/09195286
; Patent No. 6066474
; GENERAL INFORMATION:
; APPLICANT: Marcu, Kenneth B.
; TITLE OF INVENTION: Y2H56 A STRONG IKK BINDING PROTEIN
; FILE REFERENCE: Docket No. 6066474 178-258
; CURRENT APPLICATION NUMBER: US/09/195,286
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-195-286-3

Query Match 66.5%; Score 636.8; DB 3; Length 678;
Best Local Similarity 98.9%; Pred. No. 1.4e-183;
Matches 641; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy    216 CTGGACCAGAGGACGGAAGATAAGAAAGCAGAGATTGACATCCTGGCTGCAGAGTACATC 275
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Db    151 TCCACGGTGAAGACGCTGTCTCCAGACCAGCGCGTGGAGCGCCTGCAGAAGATCCAGAAC 210

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Db    211 GCCTACAGCAAGTGCAAGGAATACAGTGACGACAAAGTGCAGCTGGCCATGCAGACCTAC 270

Qy    396 GAGATGGTGGATAAACACATTCGAAGGCTTGATGCAGACCTGGCGCGCTTTGAAGCAGAT 455
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Db    331 CTGAAGGACAAGATGGAGGGCAGTGATTTTCAAAGCTCCGGAGGGCGAGGGTTAAAAAAA 390

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